



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 99797

TO: Holly Schnizer
Location: CM1/9E09/9B01
Monday, July 28, 2003
Art Unit: 1653
Phone: 305-3722
Serial Number: 09 / 302239

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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; Entered [jdelaval 28-Jul-03 11:42]
SEQ3
ANAFLLXXLRGSLRXCKXQCSFXAXXI FDKARTKLPWISY1

; Entered [jdelaval 28-Jul-03 11:43]
SEQ4
ANGFLXXLRGSLRXCKRXILCSFXAXXI FRNXXRTROFWVS1

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:05 ; Search time 25 Seconds
(without alignments)
169.257 Million cell updates/sec

Title: SEQ3
Perfect score: 190
Sequence: 1 ANAFIXLRGSLRXCKXX.....XXARXIFDAXRTLFWISY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	86.3	466	1 KFHU7	coagulation factor
2	130	68.4	443	2 I46932	coagulation factor
3	115	60.5	407	1 KFB07	coagulation factor
4	107	56.3	492	1 EXBO	coagulation factor
5	104	54.7	488	1 EXHU	coagulation factor
6	101	53.2	461	1 JX0210	protein C (activat
7	100	52.6	461	1 S18994	protein C (activat
8	98	51.6	482	1 EXRT	coagulation factor
9	97	51.1	475	1 EXCH	coagulation factor
10	96	50.5	456	1 KXBO	protein C (activat
11	88	46.3	461	1 KFHU	coagulation factor
12	87	45.8	416	1 KFB0	coagulation factor
13	86	45.3	461	1 KXHU	protein C (activat
14	85	44.7	612	1 KXHU	protein C (activat
15	81	42.6	617	1 T10511	thrombin (EC 3.4.2
16	81	42.6	618	2 A35827	thrombin (EC 3.4.2
17	79	41.6	452	1 A30351	coagulation factor
18	79	41.6	459	2 J00419	coagulation factor
19	75	39.5	642	2 S53433	plasma protein S p
20	70	36.8	642	2 S53434	plasma protein S p
21	70	36.8	676	1 KXHU	plasma protein S p
22	68	35.8	675	1 KXBO	plasma protein S p
23	66	34.7	396	1 KXBO	plasma protein S -
24	66	34.7	646	2 S38819	thrombin (EC 3.4.2
25	65	34.2	625	1 T1BO	plasma protein S p
26	65	34.2	675	1 KXRTS	plasma protein S p
27	63.5	33.4	576	2 G96763	probable MAP kinase
28	61	32.1	422	1 KXHU	plasma protein Z p
29	61	32.1	673	2 A48089	growth arrest-spec

30	59	31.1	674	2 I55476	growth potentiation
31	59	31.1	678	2 B48089	growth arrest-spec
32	58	30.5	675	1 KXMS	plasma protein S p
33	57.5	30.3	594	2 D84859	probable MAP kinase
34	57.5	30.3	603	2 C96575	probable MAP kinase
35	46.5	24.5	161	2 F82637	conserved hypochet
36	45.5	23.9	516	2 H84424	probable MAP kinase
37	45	23.7	879	2 S55864	hypochetrical prote
38	44.5	23.4	455	2 C83494	probable 2-isoprop
39	44	23.2	211	2 D96996	uncharacterized lo
40	43.5	22.9	367	2 B56598	endothelial kinase
41	43.5	22.9	385	2 T15221	hypochetrical prote
42	43.5	22.9	1298	2 A48994	protein-tyrosine k
43	43.5	22.9	1363	2 I58375	protein-tyrosine k
44	43.5	22.9	1379	2 J04954	vascular endotheli
45	43	22.6	370	2 E83518	probable acyl-CoA

ALIGNMENTS

RESULT 1
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C/Species: Homo sapiens (man)
C/Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C/Accession: A28322; A23819; A31186; B31186; S63524
R/O'Hara, F.J.; Grant, F.J.; Haldean, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A/Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend
A/Reference number: A28322; MUID:87260948; PMID:3037537
A/Accession: A28322
A/Molecule type: DNA
A/Residues: 1-466 <OHA>
A/Cross-references: GB:002933; NID:9180333; PIDN:AAA51983.1; PID:9180334
R/Hagen, F.S.; Gray, C.L.; O'Hara, F.J.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A/Title: Characterization of a cDNA coding for human factor VII.
A/Reference number: A23819; MUID:86205965; PMID:3486420
A/Accession: A23819
A/Molecule type: mRNA
A/Residues: 1-466 <HAG>
A/Cross-references: GB:M12322; NID:91827799; PIDN:AAA8040.1; PID:9182801
R/Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A/Title: Amino acid sequence and posttranslational modifications of human factor VII-a f
A/Reference number: A90539; MUID:89088153; PMID:3264725
A/Accession: A31186
A/Molecule type: protein
A/Residues: 61-212 <THI>
A/Accession: B31186
A/Molecule type: protein
A/Residues: 213-466 <TH2>
R/Bjorn, S.; Foster, D.C.; Thim, L.; Wibe, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Biol. Chem. 266, 11051-11057, 1991
A/Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A/Reference number: A40529; MUID:91250411; PMID:1904059
R/Persson, E.; Petersen, L.C.
Eur. J. Biochem. 234, 293-300, 1995
A/Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A/Reference number: S63524; MUID:96096752; PMID:8529655
A/Accession: S63524
A/Molecule type: protein
A/Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C/Genetics:
A/Gene: GDB:F7
A/Cross-references: GDB:119897; OMIM:227500
A/Map position: 13q34-13q34
A/Intons: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
C/Function:
A/Description: catalyzes the proteolytic activation of coagulation factor X in the presen
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamic
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-60/Domain: propeptide #status predicted <PRO>
F:45-104/Domain: Gla domain homology <GLA>
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:110-141/Domain: EGF homology <EG1>
F:151-187/Domain: EGF homology <EG2>
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:213-447/Domain: trypsin homology <TRY>
F:66-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:67-82,110-121,115-130,132-141,151-162,156-172,174-187,195-322,219-224,238-254,370-389,
F:112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent
F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:212-213/Cleavage site: Arg-11e (coagulation factor X1a) #status experimental
F:253,302,404/Active site: His, Asp, Ser #status predicted
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 86.3%; Score 164; DB 1; Length 466;
Best Local Similarity 75.0%; Pred. No. 2, 8e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGLXKXCKXQCSFYXARXIFPDARTKLFWISY 44
Db 61 ANAFLEELRPGSLERCKEELCSFEAREIRFPDARTKLFWISY 104

RESULT 2
coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: I46932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: I46933; MUID:93190306; PMID:8383365
A:Accession: I46932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-443 <BRO>
A:Cross-references: GB:S56300; NID:9266294; PID:9266295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
F:24-83/Domain: Gla domain homology <GLA>
F:89-120/Domain: EGF homology <EG1>
F:130-166/Domain: EGF homology <EG2>
F:192-425/Domain: trypsin homology <TRY>

Query Match 68.4%; Score 130; DB 2; Length 443;
Best Local Similarity 56.8%; Pred. No. 2e-14; Indels 15; Gaps 0;
Matches 25; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGLXKXCKXQCSFYXARXIFPDARTKLFWISY 44
Db 40 ANAFLEELRPGSLERCKEELCSFEAREIRFPDARTKLFWISY 83

RESULT 3
coagulation factor VIIa (BC 3.4.21.21) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C:Accession: A31979; C20274
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.
J. Biol. Chem. 263, 14868-14877, 1988
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.
A:Reference number: A31979; MUID:89008362; PMID:3045954
A:Accession: A31979
A:Molecule type: protein
A:Residues: 1-407 <TAK>
R:McMullen, B.W.; Fujikawa, K.; Kisiel, J. W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Accession: C20274
A:Molecule type: protein
A:Residues: 58-62, 'X', 64-68 <MCN>
A>Note: The residue designated 'X' was determined to be hydroxyaspartic acid
R:Hase, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,
J. Biochem. 104, 867-868, 1988
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A:Reference number: A4556; MUID:89213999; PMID:3149637
A:Accession: A4556
A:Contents: annotation
A:Note: structure and location of covalently bound carbohydrate
C:Function:
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen
ulation factor IX in the presence of calcium and tissue factor
A:Pathway: blood coagulation extrinsic pathway
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>
F:1-44/Domain: Gla domain homology (fragment) <GLA>
F:50-81/Domain: EGF homology <EG1>
F:91-127/Domain: EGF homology <EG2>
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
F:153-387/Domain: trypsin homology <TRY>
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxylglutamic acid (Glu) #status
F:17-22,50-61,55-70,72-81,91-102,112-114,127,135-262,159-164,178-194,310-329,340-368/
F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment
F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:152-153/Cleavage site: Arg-11e (coagulation factor X1a) #status experimental
F:193,242,344/Active site: His, Asp, Ser #status predicted
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 60.5%; Score 115; DB 1; Length 407;
Best Local Similarity 50.0%; Pred. No. 7.1e-12;
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGLXKXCKXQCSFYXARXIFPDARTKLFWISY 44
Db 1 ANAFLEELRPGSLERCKEELCSFEAREIRFPDARTKLFWISY 44

RESULT 4
EXBO
coagulation factor Xa (EC 3.4.21.6) precursor - bovine
N:Alternate names: Stuart factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
C:Accession: A22867; A14997; A12030; A34412; S39414; A00925
R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
A:Reference number: A22867; MUID:84247315; PMID:6330671
A:Accession: A22867
A:Molecule type: mRNA
A:Residues: 1-487 <FUN>
A:Cross-references: GB:X00673; NID:g192; PID:CAA2286.1; PID:g193
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
Biochemistry 19, 659-667, 1980
A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
A:Reference number: A14997; MUID:80130563; PMID:6766735
A:Accession: A14997
A:Molecule type: protein
A:Residues: 41-102, 'N', 104-180 <ENF>
R:McMullen, B.A.; Fujikawa, K.; Kisiel, J. W.
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
A:Reference number: A20274; MUID:83308813; PMID:6688526
A:Contents: annotation; revision to residue 103
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.

F:215,291,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:254,300,402/Active site: His, Asp, Ser #status predicted
Query Match 52.6%; Score 100; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 3.1e-09;
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRQGSILXKCKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 42 ANSFLSEVRAGSLRECEMEICDFEENQEIFQNVEDTLAFWIKY 85
RESULT 8
EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000
C:Accession: S49075; J04670; P50191; P50190; I62745
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra-
A:Reference number: A58498; MUID:96093366; PMID:8578533
A:Accession: S49075
A:Molecule type: mRNA
A:Residues: 1-482 <STAL>
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A:Note: submitted to the EMBL Data Library, June 1994
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A:Reference number: J04670; MUID:96194815; PMID:8647460
A:Accession: J04670
A:Molecule type: mRNA
A:Residues: 1-482 <STAL>
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601
A:Experimental source: Cos-1 cell
R:Enjuoli, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma
A:Reference number: P50190; MUID:92041742; PMID:1718949
A:Accession: P50191
A:Molecule type: protein
A:Residues: 41-58, 'X', 60-65 <ENJ1>
A:Accession: P50190
A:Molecule type: protein
A:Residues: 181-186, 'X', 188-207 <ENJ2>
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of
A:Reference number: I46196; MUID:94222160; PMID:8168596
A:Accession: I46196
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 295-383 'G', 385-455 <MTR>
A:Molecule type: DNA
A:Cross-references: GB:D21215; NID:G415309; PIDN:BA04756.1; PID:G455396
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-40/Domain: propeptide #status predicted <PRO>
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-164/Domain: EGF homology <EG2>
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>
F:183-221/Domain: activation peptide #status predicted <APT>
F:233-462/Product: coagulation factor Xa heavy chain #status predicted <ACT>
F:233-460/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:187/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status
F:274,320,417/Active site: His, Asp, Ser #status predicted
Query Match 51.6%; Score 98; DB 1; Length 482;
Best Local Similarity 40.9%; Pred. No. 7.2e-09;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRQGSILXKCKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 41 ANSFLSEVRAGSLRECEMEICDFEENQEIFQNVEDTLAFWIKY 84
RESULT 9
EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: S15838; S20380; S20381
R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Nagai,
FEBS Lett. 283, 281-285, 1991
A:Title: Primary structure of the virus activating proteinase from chick embryo. Its identity
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Molecule type: not compared with conceptual translation
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:Cross-references: DDBJ:J00844; NID:G222869; PIDN:BA00724.1; PID:G222870
R:Gotoh, B.; Yamachi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <G02>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <G0T>
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of
A:Pathway: blood coagulation
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-40/Domain: propeptide #status predicted <PRO>
F:25-84/Domain: Gla domain homology <GLA>
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>
F:90-121/Domain: EGF homology <EG1>
F:129-167/Domain: EGF homology <EG2>
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>
F:186-240/Domain: activation peptide #status predicted <APT>
F:241-475/Product: coagulation factor Xa heavy chain #status experimental <ACT>
F:241-468/Domain: trypsin homology <TRY>
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #status
F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,423
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:136,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:282,328,425/Active site: His, Asp, Ser #status predicted
Query Match 51.1%; Score 97; DB 1; Length 475;
Best Local Similarity 40.9%; Pred. No. 1.1e-08;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
Qy 1 ANAFLLXLRQGSILXKCKXQCSFXXARXIFKDAKRTKLFWISY 44
Db 41 ANSFLSEVRAGSLRECEMEICDFEENQEIFQNVEDTLAFWIKY 84
RESULT 10

A:Molecule type: mRNA
 A:Residues: 1-12, 'S', '14-73', 'P', '75-82', 'K', '84-203', 'P', '205-216', 'G', '218-298', 'A', '299-356', 'A', 'A';
 A:Cross-references: GB:J00136; NID:g182608; PIDN:AAA98126.1; PID:g182609
 A:Experimental source: liver
 R:Tharakan, V.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 58, 21-29, 1990
 A:Title: Development of an immunospecific process for factor IX purification.
 A:Reference number: A60486; MUID:90194857; PMID:2316207
 A:Accession: A60486
 A:Molecule type: protein
 A:Residues: 47-52, 'XX', '55-60', 'X', '62', 'XX', '65' <THA>
 R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:63308813; PMID:6688526
 A:Accession: A20274
 A:Molecule type: protein
 A:Residues: 105-109, 'X', '111-115' <MCM>
 R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall
 Eur. J. Biochem. 172, 565-572, 1988
 A:Title: Characterisation of two differently processed forms of human recombinant factor
 A:Reference number: S02527; MUID:86166735; PMID:3280312
 A:Accession: S02527
 A:Molecule type: protein
 A:Residues: 29-63 <BAL>
 A:Note: processed forms expressed in recombinant system
 R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dieterle, A.; Faure, T.; Meullen
 EMBO J. 9, 3255-3301, 1990
 A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice an
 A:Reference number: S12058; MUID:9106024; PMID:2209546
 A:Accession: S12058
 A:Molecule type: mRNA; protein
 A:Residues: 1-68 <JAL>
 A:Note: processed forms expressed in recombinant system
 R:Handford, P.A.; Barton, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbe
 EMBO J. 9, 475-480, 1990
 A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A:Reference number: S12377; MUID:90151623; PMID:2406129
 A:Accession: S12377
 A:Molecule type: protein
 A:Residues: 92-130 <HAN>
 A:Note: NMR detection of calcium binding by domain expressed in recombinant system
 R:de la Salle, C.; Charmanter, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-377, 1993
 A:Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A:Reference number: I59612; MUID:9405330; PMID:8236150
 A:Accession: I59612
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 444-461 <RES>
 A:Cross-references: GB:S66752; NID:g439773; PIDN:AA828588.1; PID:g439774
 R:Stoffel, E.S.; Koebert, D.D.; Sankar, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A:Title: Genomic amplification with transcript sequencing.
 A:Reference number: I59529; MUID:88127096; PMID:3340835
 A:Accession: I59529
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 290-359 <RE2>
 A:Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin
 A:Reference number: A54255; MUID:94227047; PMID:8172892
 A:Accession: A54255
 A:Molecule type: protein
 A:Residues: 'V', '204', 'X', '206-211', '212', 'D', '214', 'X', '216-221', 'D' <AGA>
 A:Note: the residues designated 'x' were determined to be threonine bound to carbohydrate
 R:Di Scipio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509; PMID:655613
 A:Contents: annotation; activation; active site; carbohydrate binding

R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 66(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Accession: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.B.
 J. Biol. Chem. 259, 5698-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; MUID:84185715; PMID:6425256
 A:Accession: A37543
 A:Contents: annotation; calcium binding
 R:Morita, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.B.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Accession: A37544
 A:Contents: annotation; calcium binding, correction
 R:Benley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A:Reference number: A37545; MUID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Sheniro, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
 A:Reference number: A30622; MUID:90078229; PMID:2592373
 A:Contents: annotation; sequence of mutant B(M) Nagoya
 A:Note: carboxylation, glycosylation, and cleavage sites
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee
 submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str
 C:Genetics:
 A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Intons: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamu
 F:1-28/Domain: signal sequence #status experimental <SIG>
 F:29-46/Domain: propeptide #status experimental <PPT>
 F:31-91/Domain: Gla domain homology <GLA>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <AUC>
 F:97-128/Domain: EGF homology <EGF>
 F:134-170/Domain: EGF homology <EG1>
 F:137-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-454/Domain: trypsin homology <TRY>
 F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #st
 F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-235,252-268,382-396,407-435/Di
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:191-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental
 F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 46.3%; Score 88; DB 1; Length 461;
 Best Local Similarity 45.7%; Pred. No. 3.6e-07;
 Matches 16; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 10 QGSLRXCKXQCSFXXARXIFKXARKLFWISY 44
 Db 57 QGDLRCKMEKCSFEBARVFNTERITRPMQY 91
 RESULT 12
 KFBQ
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine

Matches 18; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

1 ANAFLXXLRGSLXRXCKXQCSFXXRXIFKAXRTRKLM 41
 Db 43 ANSFLEBRHSSLEBCEIEETCDPEAKETIFONVDTLAFM 83

RESULT 14

TBMU

thrombin (EC 3.4.21.5) precursor [validated] - human

N/Alternate names: coagulation factor II

N/Contains: prothrombin

C/Species: Homo sapiens (man)

C/Date: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000

C/Accession: A29351, A00914, E00914, A37549, A37550, I51552

R/Degen, S.J.F.; Davie, E.W.

Biochemistry 26, 6165-6177, 1987

A/Title: Nucleotide sequence of the gene for human prothrombin.

A/Reference number: A29351, MUID:88077877, PMID:2825773

A/Accession: A29351

A/Molecule type: DNA

A/Residues: 1-622 <DEG>

A/Cross-references: GB:M17262, GB:M3691, NID:9558069, PIDN:AACG3054.1, PID:G339641

R/Degen, S.J.F.; MacGillivray, R.T.A.; Davie, E.W.

Biochemistry 22, 2087-2097, 1983

A/Title: Characterization of the complementary deoxyribonucleic acid and gene coding for

A/Reference number: A00914, MUID:83231469, PMID:6305407

A/Accession: A00914

A/Molecule type: mRNA

A/Residues: 8-163, 'N', 165-622 <DE2>

A/Cross-references: GB:V00595, GB:J00307, NID:G37128, PIDN:CAA23842.1, PID:G1335344

A/Accession: B00914

A/Molecule type: DNA

A/Residues: 188-311 <DE3>

R/Walz, D.A.; Hewitt-Emmett, D.; Seeger, W.H.

Proc. Natl. Acad. Sci. U.S.A. 74, 1969-1972, 1977

A/Reference number: A37549, MUID:77193964, PMID:266717

A/Accession: A37549

A/Molecule type: Protein

A/Residues: 44-118, 'N', 120, 'S', 122-163, 'T', 165-175, 'A', 177-182, 'T', 184-193, 'W', 196-308, 'R', Butkowski, R.J.; Elton, J.; Downing, M.R.; Mann, K.G.

J. Biol. Chem. 252, 4942-4957, 1977

A/Title: Primary structure of human prothrombin 2 and alpha-thrombin.

A/Reference number: A37550, MUID:77207112, PMID:873923

A/Accession: A37550

A/Molecule type: protein

A/Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-490, 'R', Rabier, M.J.; Blashill, A.; Furtle, B.; Furtle, B.C.

J. Biol. Chem. 261, 13210-13215, 1986

A/Reference number: A37551, MUID:8708532, PMID:3759958

A/Contents: annotation; activation cleavages

R/McGillivray, R.T.; Irwin, D.M.; Gunto, E.R.; Stone, J.C.

Ann. N. Y. Acad. Sci. 485, 73-79, 1986

A/Title: Recombinant genetic approaches to functional mapping of thrombin.

A/Reference number: I51952, MUID:87182874, PMID:3471151

A/Accession: I51952

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-2, 'R', 5-100 <RES>

A/Cross-references: GB:M3031, NID:G190723, PIDN:AAA60220.1, PID:G190724

C/Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin; can be removed either by factor Xa or thrombin; the cleavage into light and heavy chains 314-Arg, are released in natural blood clotting.

C/Comment: The cleavage after Arg-198, observed in vitro, does not occur in plasma.

C/Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy ent interaction with the negatively charged phospholipid membrane surface.

C/Comment: The prothrombin precursor is synthesized in the liver.

C/Genetic8:

A/Gene: GDB:F2

A/Cross-references: GDB:119894, OMIM:176930

A/Map position: 11p11-11q12

A/Intons: 27/1, 80/3, 89/1, 106/1, 141/2, 187/1, 292/1, 335/1, 377/2, 433/2, 491/2, 552

C/Superfamily: thrombin, Gla domain homology; kringle homology; trypsin homology

C/Keywords: acute phase; blood coagulation; calcium binding; carboxylglutamic acid; dupli

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-43/Domain: propeptide #status predicted <PRO>

F/28-87/Domain: Gla domain homology <GLA>

F/44-622/Product: prothrombin #status experimental <MAT>

F/44-327/Domain: activation peptide #status experimental <APT>

F/108-186/Domain: kringle homology <KR1>

F/213-291/Domain: kringle homology <KR2>

F/328-363/Product: thrombin light chain #status experimental <LCH>

F/364-622/Product: thrombin heavy chain #status experimental <HCH>

F/364-613/Domain: trypsin homology <TRY>

F/49, 50, 57, 59, 62, 63, 68, 69, 72, 75/Modified site: gamma-carboxylglutamic acid (Glu) #status

F/60-65, 90-103, 108-186, 129-169, 157-181, 213-291, 234-274, 262-286/Disulfide bonds: #status

F/121, 143/Binding site: carbonyl (Asn) (covalent) #status predicted

F/336-482, 536-550, 564-584/Disulfide bonds: #status predicted

F/391-407/Disulfide bonds: #status experimental

F/406, 462/Active site: His, Asp #status predicted

F/416/Binding site: carboxylate (Asn) (covalent) #status experimental

F/568/Active site: Ser #status experimental

Query Match 44.7%; Score 85; DB 1; Length 622;

Best Local Similarity 36.4%; Pred. No. 1, 6e-06;

Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

1 ANAFLXXLRGSLXRXCKXQCSFXXRXIFKAXRTRKLM 44
 Db 44 ANSFLEBRHSSLEBCEIEETCDPEAKETIFONVDTLAFM 87

RESULT 15

S10511

thrombin (EC 3.4.21.5) precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 07-May-1993 #sequence revision 07-May-1993 #text change 03-May-2002

C/Accession: S10511, A60576, B42696

R/Dhanich, M.; Monard, D.

Nucleic Acids Res. 18, 4251, 1990

A/Title: cDNA sequence of rat prothrombin.

A/Reference number: S10511, MUID:90332426, PMID:2377469

A/Accession: S10511

A/Molecule type: mRNA

A/Residues: 1-617 <DIH>

A/Cross-references: EMBL:X52835, NID:9556969, PIDN:CAA37017.1, PID:956970

R/Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.

Endocrinology 126, 167-175, 1990

A/Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.

A/Reference number: A60576, MUID:90091942, PMID:2293980

A/Accession: A60576

A/Molecule type: protein

A/Residues: 44-58 <HEN>

A/Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uterus

R/Banfield, D.K.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992

A/Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq

A/Reference number: A42696, MUID:92212913, PMID:1557383

A/Accession: B42696

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 383-617, 'E', <BAN>

A/Cross-references: GB:M81397

C/Superfamily: thrombin, Gla domain homology; kringle homology; trypsin homology

C/Keywords: blood coagulation; calcium binding; carboxylglutamic acid; glycoprotein; hydr

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-43/Domain: propeptide #status predicted <PRO>

F/28-88/Domain: Gla domain homology <GLA>

F/44-617/Product: prothrombin #status experimental <PMAT>

F/109-187/Domain: kringle homology <KR1>

F/215-292/Domain: kringle homology <KR2>

F/360-609/Domain: trypsin homology <TRY>

F/50, 51, 58, 60, 63, 64, 69, 70, 73, 76/Modified site: gamma-carboxylglutamic acid (Glu) #status

F/61-66, 91-104, 109-187, 130-170, 158-182, 215-292, 236-276, 264-287, 332-478, 387-403, 532-546, 5

F/402, 458, 564/Active site: His, Asp, Ser #status predicted

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:12:00 ; Search time 13.5 Seconds
(without alignments)
153.272 Million cell updates/sec

Title: SEQ3
Perfect score: 190
Sequence: 1 ANAFLLXRLRGSLRXCKXX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	86.3	466	FA7_HUMAN	P08709 Homo sapien
2	130	68.4	444	FA7_RABIT	P88139 oryctolagus
3	119	62.6	446	FA7_MOUSE	P70375 mus musculus
4	115	60.5	407	FA7_BOVIN	P22457 bos taurus
5	107	56.3	492	FA10_BOVIN	P00743 bos taurus
6	106	55.8	459	PRTC_PIG	O991P2 sus scrofa
7	105	55.3	218	TMG1_HUMAN	O14668 homo sapien
8	104	54.7	488	FA10_HUMAN	P00742 homo sapien
9	101	53.2	461	PRTC_MOUSE	P33587 mus musculus
10	100	52.6	461	PRTC_RAT	P13394 rattus norv
11	100	52.6	490	FA10_RABIT	O19045 oryctolagus
12	97	51.1	475	FA10_CHICK	P25155 gallus gall
13	96	50.5	456	PRTC_BOVIN	P00745 bos taurus
14	94	49.5	231	TMG3_HUMAN	O9bzd7 homo sapien
15	88	46.3	461	FA9_HUMAN	P00741 bos sapien
16	87	45.8	416	FA9_BOVIN	P00741 bos taurus
17	86	45.3	458	PRTC_RABIT	O28661 oryctolagus
18	86	45.3	461	PRTC_HUMAN	P04070 homo sapien
19	85	44.7	622	THRB_HUMAN	P00734 homo sapien
20	84	44.2	376	FA10_TROCA	P1428 troglodytis
21	81	42.6	202	TMG2_HUMAN	O14668 homo sapien
22	81	42.6	617	THRB_RAT	P18297 rattus norv
23	81	42.6	618	THRB_MOUSE	P19221 mus musculus
24	79	41.6	452	FA9_CANFA	P19540 canis famli
25	79	41.6	459	FA9_MOUSE	P16294 mus musculus
26	74.5	39.2	226	TMG4_HUMAN	O9bzd6 homo sapien
27	70	36.8	649	PRTS_MACMU	O28520 macaca mula
28	70	36.8	676	PRTS_HUMAN	P07222 bos sapien
29	68	35.8	675	PRTS_BOVIN	P07222 bos taurus
30	66	34.7	396	PRTZ_BOVIN	P00744 bos taurus
31	66	34.7	646	PRTS_RABIT	P88118 oryctolagus
32	65	34.2	625	THRB_BOVIN	P00733 bos taurus
33	65	34.2	675	PRTS_RAT	P53813 rattus norv

34	61	32.1	400	1	PRTZ_HUMAN	P22891 homo sapien
35	58	30.5	675	1	PRTS_MOUSE	O08761 mus musculus
36	45	23.7	879	1	YN65_YEAST	P42837 saccharomyc
37	44	23.2	2812	1	ZAN_HUMAN	O9y493 homo sapien
38	43.5	22.9	1298	1	VGR3_HUMAN	P35916 homo sapien
39	43.5	22.9	1363	1	VGR3_MOUSE	P35917 mus musculus
40	42.5	22.4	322	1	YOL3_CAEEL	O09292 caenorhabdi
41	42	22.1	263	1	PFLA_STRMU	O68575 streptococc
42	42	22.1	517	1	GUAA_VIBPA	O87807 vibrio para
43	42	22.1	1356	1	PAD3_HUMAN	O88w0 homo sapien
44	41.5	21.8	271	1	MD12_YEAST	O92328 saccharomyc
45	41.5	21.8	1348	1	VGR2_COTUA	P52583 coturnix co

ALIGNMENTS

RESULT 1
FA7_HUMAN STANDARD; PRT; 466 AA.
ID_ FA7_HUMAN
AC P08709; O14339;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Bptacog alfa).
GN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=86205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C., Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K., Dave E.W.;
RA "Characterization of a cDNA coding for human factor VII."; Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RL
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y., Hagen F.S., Murray M.J.;
RA "Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent protein participating in blood coagulation."; Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RL
RN [3]
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjorn S., Christensen M., Nicolsen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;
RA "Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells."; Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjorn S., Foster D.C., Thim L., Wberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kistiel W.;
RA "Human plasma and recombinant factor VII. Characterization of O-glycosylations at serine residues 52 and 60 and effects of site-directed mutagenesis of serine 52 to alanine."; J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=9062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.,
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.",
 RL *J. Biol. Chem.* 264:20320-20325(1989).
 RN [17]
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.,
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.",
 RL *Adv. Exp. Med. Biol.* 281:121-131(1990).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=96175641; PubMed=8598993;
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
 RA Kottigberg W.H., Nemerson Y., Kirchhofer D.,
 RT "The crystal structure of the complex of blood coagulation factor
 RT VIIa with soluble tissue factor.",
 RL *Nature* 380:41-46(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RX MEDLINE=99126538; PubMed=923787;
 RA Zhang B., St Charles R., Tulinsky A.,
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPI mutant.",
 RL *J. Mol. Biol.* 285:2089-2104(1999).
 RN [10]
 RP STRUCTURE BY NMR OF 105-145.
 RX MEDLINE=98367502; PubMed=9692950;
 RA Muranyi A., Flinn B.E., Gipeert G.P., Forssen S., Stenflo J.,
 RA Driksenberg T.,
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.",
 RL *Biochemistry* 37:10605-10615(1998).
 RN [11]
 RP VARIANT GLN-364.
 RX MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.,
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.",
 RL *Blood* 78:132-140(1991).
 RN [12]
 RP VARIANTS GLN-364 AND PHE-370.
 RX MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Rodozigo G., Casonato A., Girolami A., Bernardi F.,
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).",
 RL *Hum. Genet.* 89:497-502(1992).
 RN [13]
 RP VARIANT TYR-238.
 RX MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrari M., Patrascchini P., Redaelli R., Bernardi F.,
 RT "A missense mutation (178Gys-->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.",
 RL *Hum. Mol. Genet.* 2:1055-1056(1993).
 RN [14]
 RP VARIANTS.
 RX MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kempall-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnelli D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.,
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.",
 RL *Hum. Mol. Genet.* 2:1355-1359(1993).
 RN [15]
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;
 RA Chating S., Clarke B., Sridhara S.,
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.,
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.",
 RL *Blood* 83:3524-3535(1994).
 RN [16]
 RP VARIANT VAL-354.
 RX MEDLINE=96072589; PubMed=7981691;
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.,
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).",
 RL *Hum. Mol. Genet.* 3:1175-1177(1994).
 RN [17]
 RP VARIANT MET HIS-307.
 RX MEDLINE=95064662; PubMed=7974346;
 RA Ohlwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.,
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.",
 RL *Thromb. Haemost.* 71:773-777(1994).
 RN [18]
 RP VARIANT MET-419.
 RX MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.,
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.",
 RL *Blood* 87:5085-5094(1996).
 RN [19]
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RX MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Castaman G., Pinotti M., Ferrarese P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.,
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.",
 RL *Hum. Mutat.* 8:108-115(1996).
 RN [20]
 RP VARIANT VAL-304.
 RX MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Koroletishevsky M.,
 RA Zaitov R., Seligsohn U.,
 RT "A1a24Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.",
 RL *Thromb. Haemost.* 76:283-291(1996).
 RN [21]
 RP VARIANT MORIOKA PRO-13.
 RX MEDLINE=98235713; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragawa N.,
 RT "Factor VII Moriooka (P11 L-26P): a homozygous missense mutation in
 RT the signal sequence identified in a patient with factor VII
 RT deficiency.",
 RL *Br. J. Haematol.* 101:47-49(1998).
 RN [22]
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RX MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.,
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.",
 RL *Hum. Mutat. Suppl.* 1:S189-S191(1998).
 RN [23]
 RP VARIANTS ASP-295 AND GLN-413.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Althuler D., Ireland J., Sklar P., Ardile K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesi J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.,
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.",
 RL *Nat. Genet.* 22:231-238(1999).

Query Match 86.3%; Score 164; DB 1; Length 466;
 Best Local Similarity 75.0%; Pred. No. 6,8e-22;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRKCXXQCSFXXARXIFKDAKRTKFWISY 44
 DB 61 ANAFLEELRPGSLERECKECSFEAREIFKDAERTKLFWISY 104

RESULT 2
 ID FA7 RABIT STANDARD; PRT; 444 AA.
 AC P98139; P79224;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
 GN F7.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93190306; PubMed=8383365;
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."
 RL Thromb. Res. Suppl. 69:231-238 (1993).
 RN [2]
 RP REVISION TO 395.
 RC TISSUE=Liver;
 RA Ritz S.R., Blajchman M.A., Clarke B.J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
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 CC
 DR EMBL; U74777; AAB37326.1; -
 DR HSSP; P08709; 1PAK.
 DR MEROPS; S01.215; -
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla_1.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFBLD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA_1.
 DR SMART; SM00069; GLA_1.
 DR SMART; SM00020; TRY_3PC_1.
 DR PROSITE; PS00010; ASX_HYDROXYL_1.
 DR PROSITE; PS00022; EGF_1_1.
 DR PROSITE; PS01186; EGF_2_1.
 DR PROSITE; PS01187; EGF_CA_1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION_1.
 DR PROSITE; PS00240; TRYPSIN_DOM_1.
 DR PROSITE; PS00134; TRYPSIN_HIS_1.
 DR PROSITE; PS00135; TRYPSIN_SER_1.
 KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 21
 FT PROPEP 22 39
 FT CHAIN 40 191
 FT CHAIN 192 444
 FT DOMAIN 45 74
 FT DOMAIN 85 121
 FT DOMAIN 126 167
 FT DOMAIN 192 444
 FT SITE 191 192
 FT ACT_SITE 232 232
 FT ACT_SITE 281 281
 FT ACT_SITE 383 383
 FT BINDING 377 377
 FT DISULFID 56 61
 FT DISULFID 89 100
 FT DISULFID 94 109
 FT DISULFID 111 120
 FT DISULFID 130 141
 FT DISULFID 137 151
 FT DISULFID 153 166
 FT DISULFID 174 301
 FT DISULFID 198 203
 FT DISULFID 217 233
 FT DISULFID 349 368
 FT DISULFID 379 407
 FT MOD_RES 45 45
 FT MOD_RES 46 46
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 FT MOD_RES 64 64
 FT MOD_RES 65 65
 FT MOD_RES 68 68
 FT MOD_RES 74 74
 FT MOD_RES 102 102
 FT MOD_RES 211 211
 FT CARBOHYD 242 242
 FT CARBOHYD 306 306
 SO SEQUENCE 444 AA; 49011 MW; 0481ABCFB5427F8 CRC64;

Query Match 68.4%; Score 130; DB 1; Length 444;
 Best Local Similarity 56.8%; Pred. No. 9,4e-16;
 Matches 25; Conservative 4; Mismatches 15; Indels 0; Gaps 0;
 QY 1 ANAFLLXLRQGSILRKCXXQCSFXXARXIFKDAKRTKFWISY 44
 DB 40 ANAFLEELRPGSLERECKEELCSFEARIEVFQSTERTKQFWITY 83

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RESULT 3
ID FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
DE F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127167; PubMed=8972017;
RA Idusoglu E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964 (1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA OR
CC AND CALCIUM IONS. FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PMW: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U66079; AAC3796.1; -.
DR HSSP; P08709; 1BF9.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYLA; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01187; EGF_CA; 1.
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DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76
FT DOMAIN 87 123
FT DOMAIN 128 149
FT DOMAIN 194 446
FT SITE 193 194
FT ACT_SITE 234 234
FT ACT_SITE 283 283
FT ACT_SITE 385 385
FT BINDING 379 379
FT DISULFID 58 63
FT DISULFID 91 102
FT DISULFID 96 111
FT DISULFID 113 122
FT DISULFID 132 143
FT DISULFID 139 153
FT DISULFID 155 168
FT DISULFID 176 303
FT DISULFID 200 205
FT DISULFID 219 235
FT DISULFID 351 370
FT DISULFID 381 409
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
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FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 76 76
FT MOD_RES 104 104
FT MOD_RES 186 186
FT CARBOHYD 244 244
SQ SEQUENCE 446 AA; 50276 MW; 2512844A45C9C96E CRC64;

Query Match 62.6%; Score 119; DB 1; Length 446;
Best Local Similarity 56.8%; Pred. No. 9.3e-14;
Matches 25; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRGSLRKCKKXQCSFXKXKFKKXKRLKFWISY 44
Db 42 ANSLLELWPGSLERECNEQCSFEARELIFKSPERTKQFWIYV 85

RESULT 4
ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
DE accelerator).
DE F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
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RP SEQUENCE.
 RX MEDLINE=69008362; PubMed=1049594;
 RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
 RA Iwanaga S.,
 RT "Bovine factor VII. Its purification and complete amino acid
 RT sequence.";
 RL J. Biol. Chem. 263:14868-14877(1988).
 RN [2]
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.
 RX MEDLINE=9213999; PubMed=3149637;
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
 RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.,
 RT "A new trisaccharide sugar chain linked to a serine residue in bovine
 RT blood coagulation factors VII and IX.";
 RL J. Biochem. 104:867-868(1988).
 RN [3]
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RL Adv. Exp. Med. Biol. 281:121-131(1990).
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
 CC form factor Xa.
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
 CC BY A DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC PIR: A31979; KPE07.
 DR HSP, P08709; 1BF9.
 DR MEROPS; S01.215; -.
 DR InterPro: IPR000152; Asx_hydroxy1.
 DR InterPro: IPR001314; Chymotrypsin.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_T1.
 DR InterPro: IPR006209; EGF_T1.
 DR InterPro: IPR002383; GLA blood.
 DR InterPro: IPR001254; Ser protease_Try.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00001; GLABLOD.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00069; Gla; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_Ca; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KM Hydrolyase: Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KM EGF-like domain; Repeat.
 FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
 FT RT 407 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 6 35 GLA-RICH.

FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 87 128 EGF-LIKE 2.
 FT DOMAIN 153 107 SERINE PROTEASE.
 FT SITE 152 153 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,
 FT FACTOR IXa, OR THROMBIN).
 FT ACT SITE 193 193 BY SIMILARITY.
 FT ACT SITE 242 242 BY SIMILARITY.
 FT ACT SITE 344 344 BY SIMILARITY.
 FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).
 FT DISULFID 17 22 BY SIMILARITY.
 FT DISULFID 50 61 BY SIMILARITY.
 FT DISULFID 55 70 BY SIMILARITY.
 FT DISULFID 72 81 BY SIMILARITY.
 FT DISULFID 91 102 BY SIMILARITY.
 FT DISULFID 98 112 BY SIMILARITY.
 FT DISULFID 114 127 BY SIMILARITY.
 FT DISULFID 135 162 BY SIMILARITY.
 FT DISULFID 159 164 BY SIMILARITY.
 FT DISULFID 178 194 BY SIMILARITY.
 FT DISULFID 310 329 BY SIMILARITY.
 FT DISULFID 340 368 BY SIMILARITY.
 FT MOD RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
 FT MOD RES 52 52 O-LINKED (GLC...)
 FT CARBOHYD 145 145 N-LINKED (GLCNAC...)
 FT CARBOHYD 203 203 N-LINKED (GLCNAC...)
 FT SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
 SQ
 Query Match 60.5%; Score 115; DB 1; Length 407;
 Best Local Similarity 50.0%; Pred. No. 4, 5e-13;
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
 QY 1 ANAFLLXRLQSGSLKRYCKXQCSFXXARXIFKDXRKLFWISY 44
 DB 1 ANGFLLEHLPLGSLERECREBELCSFEBAHEIFRNEERTRPQWVSY 44
 ID PA10 BOVIN STANDARD; PRT; 492 AA.
 AC P00743;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI TaxID=9913;
 RP SEQUENCE OF 1-487 FROM N.A.
 RX MEDLINE=84247315; PubMed=6330671;
 RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
 RT containing a prepro leader sequence.";
 RL Nucleic Acids Res. 12:4481-4492(1984).
 RN [2]
 RP SEQUENCE OF 41-180
 RX MEDLINE=80130563; PubMed=6766735;
 RA Eitfeld D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
 RA Titani K.;
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
 RT factor).";

RL Biochemistry 19:659-667(1980).
 RN [3]
 RA REVISION TO 103.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A.; Fujikawa K.; Kiesel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens."
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
 RN [4]
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
 RX MEDLINE=76053069; PubMed=1059093;
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
 RA Neurath H.;
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
 RT chain."
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
 RN [5]
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X."
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE=73053114; PubMed=4264286;
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
 RA Neurath H., Davie E.W.;
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology
 RT with mammalian serine proteases."
 RL Biochemistry 11:4899-4903(1972).
 RN [7]
 RP PROCESSING.
 RX MEDLINE=76053121; PubMed=1059122;
 RA Fujikawa K., Titani K., Davie E.W.;
 RT "Activation of bovine factor X (Stuart factor): conversion of factor
 RT Xa-alpha to factor Xa-beta."
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
 RN [8]
 RP CALCIUM-BINDING DATA.
 RX MEDLINE=84185716; PubMed=6546930;
 RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;
 RT "Calcium-binding properties of bovine factor X lacking the gamma-
 RT carboxyglutamic acid-containing region."
 RL J. Biol. Chem. 259:5705-5710(1984).
 RN [9]
 RP SUPFATION
 RX MEDLINE=86140210; PubMed=3949800;
 RA Morita T., Jackson C.M.;
 RT "Localization of the structural difference between bovine blood
 RT coagulation factors XI and X2 to tyrosine 18 in the activation
 RT peptide."
 RL J. Biol. Chem. 261:4008-4014(1986).
 RN [10]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=91084483; PubMed=2261466;
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
 RT the amino-terminal epidermal growth factor like domain in coagulation
 RT factor X."
 RL Biochemistry 29:8111-8118(1990).
 RN [11]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92329412; PubMed=1627540;
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
 RA Teleman O.;
 RT "Three-dimensional structure of the apo form of the N-terminal
 RT EGF-like module of blood coagulation factor X as determined by NMR
 RT spectroscopy and simulated folding."
 RL Biochemistry 31:5974-5983(1992).
 RN [12]
 RP STRUCTURE BY NMR OF 85-126.

RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
 RA Stenflo J., Drakenberg T.;
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X."
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunnerhagen M., Olan G.A., Stenflo J., Foren S., Drakenberg T.,
 RA Trethewella J.;
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study."
 RL Biochemistry 35:11547-11559(1996).
 CC -I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -I- PTM: N- AND O-GLYCOSYLATED.
 CC -I- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY) OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -I- SIMILARITY: Contains 2 EGF-like domains.
 CC
 CC -----
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 CC -----
 CC EMBL; X00673; CAA25286.1; -.
 CC PIR; A22867; EXBO.
 DR PDB; 1APO; 31-JAN-94.
 DR PDB; 1CCF; 31-MAY-94.
 DR PDB; 1WHE; 15-MAY-97.
 DR PDB; 1WHF; 15-MAY-97.
 DR PDB; 1IOD; 21-JAN-03.
 DR PDB; 1KIG; 28-OCT-98.
 DR MEROPS; S01.216; -.
 DR GlycoSiteDB; P00743; -.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; Gla_blood.
 DR InterPro; IPR01254; Ser_protease_Try.
 DR InterPro; IPR000294; VltK_dep_Gla.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SMO0020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Glycocyproline; Hydroxylase; Serine protease; Plasma; Blood coagulation;
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW Signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 FT SIGNAL 1 23
 FT PROPEP 24 40
 FT CHAIN 41 180
 FT CHAIN 183 492
 FT PROPEP 183 492
 FT CHAIN 234 492
 FT PROPEP 476 492
 FT DOMAIN 86 122
 FT DOMAIN 125 165
 FT DOMAIN 234 492
 FT ACT_SITE 275 275
 FT ACT_SITE 321 321
 FT ACT_SITE 418 418
 FT MOD_RES 46 46
 FT MOD_RES 47 47
 FT MOD_RES 54 54
 FT MOD_RES 56 56
 FT MOD_RES 59 59
 FT MOD_RES 60 60
 FT MOD_RES 65 65
 Query Match 56.3%; Score 107; DB 1; Length 492;
 Best Local Similarity 45.5%; Pred. No. 1.6e-11;
 Matches 20; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
 1 ANAFLLXLRGSLRXCKXCCSFXRXARXFKDXRKLPTISY 44
 41 ANSLFEEVKQGNLERCLEACSLSEARVEVDAEQDFEWSKY 84

CC strongly promoted by thrombomodulin.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: The vitamin K-dependent enzymatic carboxylation of some Glu
 CC residues allows the modified protein to bind calcium.
 CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
 CC another site, beyond the GLA domain. This GLA-independent binding
 CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
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 CC or send an email to license@isb-sib.ch).

 CC EMBL; AF191307; AAC28380.1; -
 CC HSRP; P04070; IPCU.
 CC MEROPS; S01.218; -
 CC InterPro; IPR000152; Asx_hydroxyl.
 CC InterPro; IPR001314; Chymotrypsin.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR006209; EGF_Like.
 CC InterPro; IPR002383; GLA_Blood.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR001254; Ser_protease_Try.
 CC InterPro; IPR000294; VltK_dep_GLA.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00594; GlA; 1.
 CC Pfam; PF00089; Trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00181; EGF; 2.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; TRYPSIN_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS01187; EGF_Ca; 1.
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE; PS50240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Glycocyproline; Serine protease;
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 CC EGF-like domain; Repeat; Endothelial cell; Hydroxylase; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT PEPTIDE 199 213
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RES 47 47
 FT MOD_RES 48 48
 FT MOD_RES 55 55
 FT MOD_RES 57 57
 FT MOD_RES 60 60
 FT MOD_RES 61 61

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FT MOD_RES 66 66 SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
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Query Match 55.8%; Score 106; DB 1; Length 459;
Best Local Similarity 47.7%; Pred. No. 2.2e-11;
Matches 21; Conservative 3; Mismatches 20; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRQGSILRXCKXQCSFYXARXIFKDXARTKLFWISY 44
DB 42 ANSFLEELRPSLSRECKEETCDFEAREEIFONTENTWAFMSKY 85
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RESULT 7
TMG1_HUMAN STANDARD; PRT; 218 AA.
ID TMG1_HUMAN STANDARD; PRT; 218 AA.
AC 014668;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
1).
GN PRG1 OR TMG1 OR PRG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.B., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
EMBL; AF009242; AAB67070.1; -.
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DR HSPB; P00740; ICFH.
DR Genew; HGNC:9469; PRG1.
DR MIM; 604428; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM0069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; vitamin K; Transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 1 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 21 83 PROTEIN 1.
FT TRANSMEM 84 106 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 107 218 POTENTIAL.
FT DOMAIN 124 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
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Query Match 55.3%; Score 105; DB 1; Length 218;
Best Local Similarity 43.2%; Pred. No. 1.5e-11;
Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
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Oy 1 ANAFLXLRQGSILRXCKXQCSFYXARXIFKDXARTKLFWISY 44
DB 21 ANGFEEIRQGNIERECKEETCFEAREAREENNEKTEFEWSTY 64
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RESULT 8
FA10_HUMAN STANDARD; PRT; 488 AA.
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ID FA10_HUMAN STANDARD; PRT; 488 AA.
AC P00742; O14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (BC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1902434;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
human coagulation factor X."
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kuzachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
organization is essentially identical with that of factor IX and
protein C."
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Ozuna M., Peol C.L., Toch E.J., Yi O., Nickerson D.A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
blood coagulation factor X."
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [5]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
```

RX MEDLINE=66221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA";
 RL Gene 41:311-314(1986).
 RN [6]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=6325207; PubMed=6871167;
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN [7]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=LIVER;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytue S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN [8]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:153-163(1993).
 RN [9]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusan K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=9618463;
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural basis for chemical inhibition of human blood coagulation
 RT factor Xa.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
 RN [12]
 RP VARIANTS ILE-7 AND HIS-30.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Althuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nimesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 RN [13]
 RP ERRATUM.
 RA Cargill M., Althuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nimesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Genet. 23:373-373(1999)."
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -----
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 DR EMBL; K03194; AA52490.1; -;
 DR EMBL; M57285; AA52421.1; -;
 DR EMBL; AF503510; AA019347.1; -;
 DR EMBL; L29433; AA52764.1; -;
 DR EMBL; L00390; AA52764.1; JOINED.
 DR EMBL; L00391; AA52764.1; JOINED.
 DR EMBL; L00392; AA52764.1; JOINED.
 DR EMBL; L00393; AA52764.1; JOINED.
 DR EMBL; L00394; AA52764.1; JOINED.
 DR EMBL; L00395; AA52764.1; JOINED.
 DR EMBL; L00396; AA52764.1; JOINED.
 DR EMBL; M22613; AA51984.1; -;
 DR EMBL; K01865; AA52486.1; -;
 DR EMBL; M33297; AA52636.1; -;
 DR PIR; A24478; EXRU.
 DR PDB; 1HCG; 08-MAY-95.
 DR PDB; 1FAX; 29-OCT-97.
 DR PDB; 1FXY; 17-JUN-98.
 DR PDB; 1XKA; 23-MAR-99.
 DR PDB; 1XKB; 23-MAR-99.
 DR PDB; 1EZO; 20-SEP-00.
 DR PDB; 1FOR; 20-SEP-00.
 DR PDB; 1FOS; 20-SEP-00.
 DR PDB; 1FJS; 17-NOV-00.
 DR PDB; 1G2L; 20-OCT-01.
 DR PDB; 1G2M; 20-OCT-01.
 DR PDB; 1KSN; 19-JUN-02.
 DR PDB; 1KYE; 11-FEB-03.
 DR PDB; 1MO5; 28-JAN-03.
 DR PDB; 1MO6; 28-JAN-03.
 DR PDB; 1NEU; 25-FEB-03.
 DR PDB; 1NEW; 25-FEB-03.
 DR PDB; 1NFX; 25-FEB-03.
 DR PDB; 1NFY; 25-FEB-03.
 DR MEROPS; S01.216; -;
 DR GlycoSuiteDB; P00742; -;
 DR Genew; HSCNC3528; F10.
 DR MIM; 134530; -;
 DR MIM; 227600; -;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0003804; F:Blood coagulation factor X activity; TAS.
 DR GO; GO:0007596; P:Blood coagulation; TAS.
 DR InterPro; IPR000152; Axx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_II.
 DR InterPro; IPR003383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla; 1.

FT	DISULFID	95	110	BY SIMILARITY.
FT	DISULFID	112	121	BY SIMILARITY.
FT	DISULFID	129	140	BY SIMILARITY.
FT	DISULFID	136	149	BY SIMILARITY.
FT	DISULFID	151	164	BY SIMILARITY.
FT	DISULFID	172	340	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	239	244	BY SIMILARITY.
FT	DISULFID	259	275	BY SIMILARITY.
FT	DISULFID	388	402	BY SIMILARITY.
FT	DISULFID	413	441	BY SIMILARITY.
FT	CARBOHYD	61	61	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	490 AA.	53965 MM;	3A39FA85AF2A6D11 C8C64;
Query Match				
Best Local Similarity	52.6%;	Score 100;	DB 1;	Length 490;
Matches	18;	Conservative	8;	Mismatches 18; Indels 0; Gaps 0;
Oy	1	ANAPLXLROGSLKRXCKXQCSFXKXKXIFKDAKRYLFWISY	44	
Db	41	ANSFLEELKXGNLREKCEWENCSYEALAEVFEDEKTEBFWNKY	84	
RESULT 12				
FA10	CHICK	STANDARD;	PRT;	475 AA.
AC	P25155;			
DT	01-MAY-1992	(Rel. 22, Created)		
DT	01-MAY-1992	(Rel. 22, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)			
GN	FX.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Chorioallantoic membrane;			
RX	MEDLINE=91257322; PubMed=2044767;			
RA	Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotoh B.,			
RA	Ogasawara T., Nagai Y.;			
RT	"Primary structure of the virus activating protease from chick			
RL	embryo. Its identity with the blood clotting factor Xa.";			
RN	FEBS Lett. 285:281-285(1991).			
RP	[2]			
RC	SEQUENCE OF 41-55 AND 241-261.			
RX	TISSUE=Allantoic fluid;			
RA	MEDLINE=91065352; PubMed=2174359;			
RA	Gotoh B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,			
RA	Nagai Y.;			
RT	"An endoprotease homologous to the blood clotting factor X as a			
RL	determinant of viral tropism in chick embryo.";			
EMBO	J. 9:4189-4195(1990).			
CC	-1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that			
CC	converts prothrombin to thrombin in the presence of factor Va,			
CC	calcium and phospholipid during blood clotting.			
CC	-1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENDAI VIRUS, NDV,			
CC	AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING			
CC	SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC			
CC	SAC.			
CC	-1- CATALYTIC ACTIVITY: Preferential cleavage: Arg- -Thr and then			
CC	Arg- -Ile bonds in prothrombin to form thrombin.			
CC	-1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR			
CC	BY THE EXCISION OF TWO ARG RESIDUES AND ARE HEID TOGETHER BY 1 OR			
CC	MORE DISULFIDE BONDS.			
CC	-1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.			
CC	-1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME			
CC	GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND			
CC	CALCIUM.			

CC	-1- PMT THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC	INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC	-1- SIMILARITY: Contains 2 EGF-like domain.
CC	-----
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities require a license agreement (See http://www.ebi.ac.uk/announcements/
CC	or send an email to license@ebi.ac.uk).
CC	-----
DR	EMBL; D00844; BAA00724.1; -.
DR	PIR; S15838; EXCH.
DR	HSSP; P00742; IHCG.
DR	MEROPS; S01.216; -.
DR	InterPro; IPR000152; Aex_hydroxyl.
DR	InterPro; IPR001314; Chymotrypsin.
DR	InterPro; IPR0000742; EGF 2.
DR	InterPro; IPR001881; EGF Ca.
DR	InterPro; IPR001438; EGF II.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR002383; GLA_blood.
DR	InterPro; IPR001254; Ser_protease_Try.
DR	InterPro; IPR000294; Vitk_dep_GLA.
DR	Pfam; PF00008; EGF; 2.
DR	Pfam; PF00594; gla; 1.
DR	Pfam; PF00089; trypsin; 1.
DR	PRINTS; PR00722; CHYMOTRYPSIN.
DR	PRINTS; PR00010; EGFBLD.
DR	PRINTS; PR00001; GLABLOOD.
DR	SMART; SM00179; EGF CA; 1.
DR	SMART; SM00069; GLA; 1.
DR	SMART; SM00020; Tryp_spc; 1.
DR	PROSITE; PS00010; AEX_HYDROXYL; 1.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; 2.
DR	PROSITE; PS01187; EGF CA; 1.
DR	PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW	Gamma-carboxylglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW	Signal; zymogen; EGF-like domain; Repeat.
FT	SIGNAL 1 20 OR 30, OR 31 (POTENTIAL).
FT	PROPEP 21 40
FT	CHAIN 41 180 FACTOR X LIGHT CHAIN.
FT	CHAIN 186 475 FACTOR X HEAVY CHAIN.
FT	PROPEP 186 241 ACTIVATION PEPTIDE.
FT	CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT	DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN 125 168 EGF-LIKE 2.
FT	DOMAIN 241 475 SERINE PROTEASE.
FT	MOD_RES 46 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 47 (BY SIMILARITY).
FT	MOD_RES 47 (BY SIMILARITY).
FT	MOD_RES 54 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 54 (BY SIMILARITY).
FT	MOD_RES 56 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 56 (BY SIMILARITY).
FT	MOD_RES 59 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 59 (BY SIMILARITY).
FT	MOD_RES 60 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 60 (BY SIMILARITY).
FT	MOD_RES 65 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 65 (BY SIMILARITY).
FT	MOD_RES 66 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 66 (BY SIMILARITY).
FT	MOD_RES 69 GAMMA-CARBOXYGLUTAMIC ACID
FT	MOD_RES 69 (BY SIMILARITY).


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FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 79 79 (BY SIMILARITY).
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 103 103 (BY SIMILARITY).
FT ACT_SITE 282 282 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 154 167 BY SIMILARITY.
FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
FT DISULFID 247 252 BY SIMILARITY.
FT DISULFID 267 283 BY SIMILARITY.
FT DISULFID 396 410 BY SIMILARITY.
FT DISULFID 421 449 BY SIMILARITY.
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 475 AA, 53142 MW, 570BF84956C5C74D CRC64;

Query Match 51.1%; Score 97; DB 1; Length 475;
Best Local Similarity 40.9%; Pred. No. 9.7e-10;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANAFXLXRGSLXRCCKXQCSFXKXRIFFDXMRTKLFWTSY 44
Db 41 ANSFLEMKQGNIEKNEERCSKEAREAFEDNKEETFEWNY 84

RESULT 13
PRTC_BOVIN STANDARD; PRT; 456 AA.
ID P00745;
AC 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
DE PROC.
GN Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OK NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillicray R.T.A.;
RA "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RA Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN [2]
RP SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.
RP MEDLINE=83007325; PubMed=6896876;
RA "Amino acid sequence of the light chain of bovine protein C.";
RA J. Biol. Chem. 257:12170-12179(1982).
RN [3]
RP REVISION TO 110.
RP MEDLINE=83169769; PubMed=6572939;
RA Drakenberg T., Fernlund P., Roesporoff P., Stenflo J.;
RA "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RA Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN [4]
RP SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-269; ASN-350
RP AND ASN-356.
RP MEDLINE=83007326; PubMed=6896877;
RA Stenflo J., Fernlund P.;
```

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RT "Amino acid sequence of the heavy chain of bovine protein C.";
RL J. Biol. Chem. 257:12180-12190(1982).
RN [5]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RP MEDLINE=83213513; PubMed=6904092;
RA Esmon N.L., Debault L.E., Esmon C.T.;
RA "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RA domainless protein C.";
RL J. Biol. Chem. 258:5548-5553(1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RP MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
RA "Structural changes required for activation of protein C are induced
RA by Ca2+ binding to a high affinity site that does not contain gamma-
RA carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL, K02435; AAA30685.1; -.
DR PIR, A26250; KXBO.
DR HSSP, P04070; 1PCU.
DR MEROPS, S01.218; -.
DR InterPro: IPR000152; Asx hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR002183; GLA_Blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Ser protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam, PF00008; EGF, 2.
DR Pfam, PF00594; Gla, 1.
DR Pfam, PF00089; trypsin, 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR PRINTS, PR00001; GLABLOOD.
DR SMART, SM00181; EGF, 2.
DR SMART, SM00659; GLA, 1.
DR SMART, SM00020; Tryp_Spc, 1.
DR PROSITE, PS00010; Asx_HYDROXYL, 1.
DR PROSITE, PS00022; EGF_1, 1.
DR PROSITE, PS01186; EGF_2, 1.
DR PROSITE, PS01187; EGF_CA, 1.
DR PROSITE, PS00011; GLU_CARBOXYLATION, 1.
DR PROSITE, PS50240; TRYPSIN_DOM, 1.
DR PROSITE, PS00134; TRYPSIN_HIS, FALSE_NEG.
```



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DR PROSITE; PS00135; TRYPSIN SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPEP 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 62 62
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 110 110
FT ACT_SITE 252 252
FT ACT_SITE 298 298
FT ACT_SITE 397 397
FT ACT_SITE 56 61
FT DISULFID 89 108
FT DISULFID 98 103
FT DISULFID 102 117
FT DISULFID 119 128
FT DISULFID 137 148
FT DISULFID 144 157
FT DISULFID 159 172
FT DISULFID 180 318
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136
FT CARBOHYD 289 289
FT CARBOHYD 350 350
FT CARBOHYD 366 366
FT VARIANT 82 82
FT VARIANT 82 82
FT CONFLICT 455 455
SQ SEQUENCE 456 AA; 51407 MW; 3CAF6833F894C209 CRC64;

Query Match 50.5%; Score 96; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 1.4e-09;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSLRXCKXQCSFXXARXIFKDAKRTKLFWISY 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 40 ANSFLEELRPQNVRECESEVEFEAREIFONTEDTIAFWFSY 83

RESULT 14
TMG3 HUMAN STANDARD; PRT; 231 AA.
AC Q9B2D7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;

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RX MEDLINE=21117044; PubMed=11171957;
RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RU Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PPM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
DR EMBL; AF326350; AKK00955.1; -.
DR HSSP; P00740; ICFH.
DR GO; GO:0016021; C:integral to membrane; NMS.
DR InterPro; IPR00294; VltK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19
FT CHAIN 20 231
FT FT 19 POTENTIAL.
FT FT 20 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT 78 POTENTIAL.
FT FT 79 101 EXTRACELLULAR (POTENTIAL).
FT FT 102 231 POTENTIAL.
FT FT 23 CYTOPLASMIC (POTENTIAL).
FT FT 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MW; 8A373E48490D81 CRC64;

Query Match 49.5%; Score 94; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 1.6e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSLRXCKXQCSFXXARXIFKDAKRTKLFWISY 44
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 ANSFLEELRPQNVRECESEVEFEAREIFONTEDTIAFWFSY 63

RESULT 15
FA9 HUMAN STANDARD; PRT; 461 AA.
ID FA9 HUMAN
AC P00740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86000558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kutachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antihemophilic
RT factor B).";
RL Biochemistry 24:3736-3750(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham U.B., Stafford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
RT human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).

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[13] SEQUENCE FROM N.A.
RX MEDLINE=84236100; PubMed=6329734;
RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
RT Huddleston J.A., Brownlee G.G.;
RL "The gene structure of human anti-haemophilic factor IX";
RM BMO J. 3:1053-1060(1984).
[14] SEQUENCE FROM N.A.
RX MEDLINE=8320788; PubMed=6687940;
RA Jave M., de la Salle H., Schamber F., Bolland A., Kohl V.,
RA Pinelli A., Tolcoshev P., Lecocq J.P.;
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
RT unique 52-base synthetic oligonucleotide probe deduced from the amino
RT acid sequence of bovine factor IX";
RL Nucleic Acids Res. 11:2325-2335(1983).
[15] SEQUENCE FROM N.A., AND VARIANTS THR-194 AND PRO-461.
RA Rieder M.U., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N.R., Toch E.J., Yi Q., Nickerson D.A.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
[16] SEQUENCE OF 36-326 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=84300526; PubMed=6089357;
RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
RT "Isolation and characterization of human factor IX cDNA:
RT identification of Tag I polymorphism and regional assignment";
RL Somat. Cell Mol. Genet. 10:465-473(1984).
[17] SEQUENCE OF 290-359 FROM N.A.
RX MEDLINE=88127096; PubMed=3340835;
RA Stotler E.S., Koebel D.D., Sarkar G., Sommer S.S.;
RT "Genomic amplification with transcript sequencing";
RL Science 239:491-494(1988).
[18] SEQUENCE OF 444-461 FROM N.A.
RX MEDLINE=94054330; PubMed=826150;
RA de la Salle C., Charantier J.L., Baas M.J., Schwartz A.,
RA Wiesel M.L., Grunebaum L., Cazenave J.-P.;
RT "A deletion located in the 3' non translated part of the factor IX
RT gene responsible for mild haemophilia B";
RL Thromb. Haemost. 70:370-371(1993).
[19] SEQUENCE OF 47-461 (VARIANT NAGoya).
RX MEDLINE=90078229; PubMed=2592373;
RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
RA Ogata K., Kamaya T., Saito H., Nino Y., Iwanaga S.;
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell
RT chymase";
RL J. Biol. Chem. 264:21257-21265(1989).
[10] HYDROXYLATION OF ASP-110.
RX MEDLINE=83308813; PubMed=6688526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
[11] PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=78194509; PubMed=659613;
RA di Scipio R.G., Kurachi K., Davie E.W.;
RT "Activation of human factor IX (Christmas factor)";
RL J. Clin. Invest. 61:1528-1538(1978).
[12] CALCIUM-BINDING DATA.
RX MEDLINE=84185715; PubMed=6425296;
RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
RT "Derivatives of blood coagulation factor IX contain a high affinity
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid";
RL J. Biol. Chem. 259:5698-5704(1984).
[13]

RP ERRATUM.
RA Morita T., Isaacs B.S., Esmen C.T., Johnson A.E.;
RL J. Biol. Chem. 260:2583-2583(1985).
[14] SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=86189947; PubMed=3009023;
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;
RT "Defective propeptide processing of blood clotting factor IX caused
RT by mutation of arginine to glutamine at position -4";
RL Cell 45:343-348(1986).
[15] STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
RA Shimonishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z";
RL J. Biol. Chem. 264:20320-20325(1989).
[16] STRUCTURE OF CARBOHYDRATE ON SER-99.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z";
RL Adv. Exp. Med. Biol. 281:121-131(1990).
[17] STRUCTURE OF CARBOHYDRATE ON SER-107.
RX MEDLINE=92388094; PubMed=1517205;
RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
RT serine 61 through the fucose residue";
RL J. Biol. Chem. 267:17520-17525(1992).
[18] PHOSPHORYLATION OF SER-114.
RX Harris R.J., Papac D.I., Tuong L., Smith K.J.;
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX";
RL (In) Abstracts of Xth international conference on methods in protein
RL structure analysis, pp.50-50, Annecy (1996).
[19] POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=20575397; PubMed=1113752;
RA Arruda V.R., Hagstrom J.N., Deltch J., Helman-Patterson T.,
RA Canale R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
RA Larson P.J., High K.A.;
RT "Posttranslational modifications of recombinant myotube-synthesized
RT human factor IX";
RL Blood 97:130-138(2001).
[20] STRUCTURE BY NMR OF 47-93.
RX MEDLINE=95229607; PubMed=7713897;
RA Freedman S.J., Furtle B.C., Furtle B., Baleja J.D.;
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
RT binding region of factor IX by two-dimensional NMR spectroscopy";
RL J. Biol. Chem. 270:7980-7987(1995).
[21] STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96032604; PubMed=7547952;
RA Freedman S.J., Furtle B.C., Furtle B., Baleja J.D.;
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
RT domain of factor IX";
RL Biochemistry 34:12126-12137(1995).
[22] STRUCTURE BY NMR OF 47-93.
RX MEDLINE=96279169; PubMed=8663165;
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furtle B.C.,
RA Furtle B.;
RT "Identification of the phospholipid binding site in the vitamin K-
RT dependent blood coagulation protein factor IX";
RL J. Biol. Chem. 271:16227-16236(1996).
[23] STRUCTURE BY NMR OF 47-93.
RP

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RX MEDLINE=97199336; PubMed=9047312;
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
RA Smith H., Hickey R.G., Pedersen L.G.;
RT "Refinement of the NMR solution structure of the
RT gamma-carboxyglutamic acid domain of coagulation factor IX using
RT molecular dynamics simulation with initial Ca2+ positions determined
RT by a genetic algorithm.";
RL Biochemistry 36:2132-2138 (1997).
[24]
RN STRUCTURE BY NMR OF 91-133.
RP MEDLINE=91306127; PubMed=1854745;
RX Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
RA "Sequence-specific 1H NMR assignments, secondary structure, and
RT location of the calcium binding site in the first epidermal growth
RT factor like domain of blood coagulation factor IX.";
RL Biochemistry 30:7402-7409 (1991).
[25]
RN STRUCTURE BY NMR OF 92-130.
RX MEDLINE=93284090; PubMed=1304885;
RA Baron M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
RA Tee A.G.D., Brownlee G.G., Campbell I.D.C.;
RT "The three-dimensional structure of the first EGF-like module of
RT human factor IX: comparison with EGF and TGF-alpha.";
RL Protein Sci. 1:81-90 (1992).
[26]
RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
RP MEDLINE=95330802; PubMed=7606779;
RX Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;

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Query Match          46.3%; Score 88; DB 1; Length 461;
Best Local Similarity 45.7%; Pred. No. 4e-08;
Matches 16; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

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QY 10 QGSIXRXCKXXQCSFXRXRXIFKDXRTKLFWISY 44
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Db 57 QGNLRECMEEKCSFEARVVFENTERTERTEFWKQY 91

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Search completed: July 28, 2003, 12:24:27
 Job time : 14.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:25 ; Search time 61 Seconds
(without alignments)
186.136 Million cell updates/sec

Title: SEQ3
Percent score: 190
Sequence: 1 ANAFLXXLRGSLRXCKXX.....XXARXIFKDXRTLFWISY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	86.3	701	4 Q96P08	Q96P08 homo sapien
2	119	62.6	446	1 Q61109	Q61109 mus musculu
3	105	55.3	268	4 Q8NEK6	Q8NEK6 homo sapien
4	105	55.3	446	11 Q8K3U6	Q8K3U6 rattus norv
5	102	53.7	443	13 Q8JHC9	Q8JHC9 brachydanio
6	101	53.2	460	11 Q91WN8	Q91WN8 mus musculu
7	98	51.6	229	13 Q8J340	Q8J340 xenopus lae
8	98	51.6	482	11 Q63207	Q63207 rattus norv
9	96	50.5	469	6 Q9GMD9	Q9GMD9 ornithorhyn
10	96	50.5	481	11 Q54740	Q54740 mus musculu
11	96	50.5	481	11 Q99L32	Q99L32 mus musculu
12	96	50.5	481	11 Q88947	Q88947 mus musculu
13	95	50.0	460	11 Q99P06	Q99P06 mus musculu
14	94	49.5	231	4 Q8N2N6	Q8N2N6 homo sapien
15	93	48.9	456	6 Q9TTR0	Q9TTR0 canis famli
16	88	46.3	456	4 Q14316	Q14316 homo sapien

17	88	46.3	461	6 Q95ND7	Q95ND7 pan troglod
18	88	46.3	461	6 Q95ND6	Q95ND6 pan troglod
19	88	46.3	474	13 Q8JHC8	Q8JHC8 brachydanio
20	87	45.8	49	6 Q95ME8	Q95ME8 bos taurus
21	85	44.7	100	4 Q15253	Q15253 homo sapien
22	82	43.2	376	13 P83370	P83370 homiocephal
23	81	42.6	179	4 Q8TAS3	Q8TAS3 homo sapien
24	81	42.6	198	11 Q8R182	Q8R182 mus musculu
25	80	42.1	138	6 Q28994	Q28994 sus scrofa
26	75	39.5	433	13 Q8JHD0	Q8JHD0 brachydanio
27	75	39.5	433	13 Q90TK1	Q90TK1 brachydanio
28	75	39.5	648	6 Q29094	Q29094 sus scrofa
29	72	37.9	55	4 Q8J002	Q8J002 homo sapien
30	72	37.9	55	4 Q8IXB5	Q8IXB5 homo sapien
31	72	37.9	399	11 Q8C101	Q8C101 mus musculu
32	72	37.9	399	11 Q9C0M3	Q9C0M3 mus musculu
33	70	36.8	98	13 P82807	P82807 notechis sc
34	70	36.8	650	4 Q16519	Q16519 homo sapien
35	70	36.8	650	4 Q9NSD0	Q9NSD0 homo sapien
36	65.5	34.5	542	5 Q8T613	Q8T613 halocynthia
37	64.5	33.9	226	11 Q8BM25	Q8BM25 mus musculu
38	64.5	33.9	226	11 Q8BGN6	Q8BGN6 mus musculu
39	63.5	33.4	431	10 Q94EY5	Q94EY5 arabidopsis
40	63.5	33.4	492	10 Q9SMJ7	Q9SMJ7 cicer ariet
41	63.5	33.4	543	10 Q9MB23	Q9MB23 arabidopsis
42	63.5	33.4	576	10 Q9C9U4	Q9C9U4 arabidopsis
43	63.5	33.4	589	10 Q9LMS2	Q9LMS2 arabidopsis
44	63	33.2	503	13 Q8AYE4	Q8AYE4 brachydanio
45	63	33.2	608	13 Q9PTW7	Q9PTW7 struthio ca

ALIGNMENTS

RESULT 1

Q96P08	PRELIMINARY;	PRT;	701 AA.
ID Q96P08			
AC Q96P08			
DT 01-DEC-2001 (TRENBERG, 19, Created)			
DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)			
DT 01-MAR-2003 (TRENBERG, 23, Last annotation update)			
DE Factor VII active site mutant immunocognate.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI Taxid=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21477448; PubMed=11593034;			
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor			
RT cells for immunotherapy in mouse models of prostatic cancer.";			
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).			
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
DR EMBL; AF272774; AKS58686.1; -			
DR HSPB; P00761; IAN1.			
DR InterPro; IPR000152; Asx_hydroxyl.			
DR InterPro; IPR001314; Chymotrypsin.			
DR InterPro; IPR000742; BGF_2.			
DR InterPro; IPR001881; BGF_Ca.			
DR InterPro; IPR001438; BGF_II.			
DR InterPro; IPR006209; BGF_like.			
DR InterPro; IPR002383; BGF_like.			
DR InterPro; IPR007110; IG-like.			
DR InterPro; IPR003597; IG-cl.			
DR InterPro; IPR003006; IG_MHC.			
DR InterPro; IPR001254; Ser_protease_Try.			
DR InterPro; IPR000294; VitK_dep_GLA.			
DR Pfam; PF00008; EGF_2.			
DR Pfam; PF00594; G1a; 1.			
DR Pfam; PF00047; IG; 2.			
DR Pfam; PF00089; trypsin; 1.			
DR PRINTS; PR00722; CHYMOTRYPSIN.			

DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00407; IGCL; 1.
 DR SMART; SM00020; TRYSP; 1.
 DR PROSITE; PS00010; ASK_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
 DR PROSITE; PS50835; IG_Like; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 86.3%; Score 164; DB 4; Length 701;
 Best Local Similarity 75.0%; Pred. No. 7e-22;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRXCKXQCSFXAXRIFKDXARTLFWISY 44
 Db 61 ANAFLEELRPGSLRECKEKEQCSFEAREIFPDARTKLFWISY 104

RESULT 2

ID 061109 PRELIMINARY; PRT; 446 AA.
 AC 061109;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Coagulation factor VII.
 DE P7 OR FVII.
 CN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96376538; PubMed=8701412;
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RT "Characterization of a cDNA encoding murine coagulation factor VII.";
 RL Thromb. Haemost. 75:481-487(1996).
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; U44795; AAC52570.1; -.
 DR HSSP; P08709; 1PAK.
 DR MGD; MGI:109325; F7.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR00152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Set_protease_Try.
 DR InterPro; IPR00294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYSP; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00010; ASK_HYDROXYL; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 RT

DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 62.6%; Score 119; DB 11; Length 446;
 Best Local Similarity 56.8%; Pred. No. 1.2e-13;
 Matches 25; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRXCKXQCSFXAXRIFKDXARTLFWISY 44
 Db 42 ANSLLEELRPGSLRECKEKEQCSFEAREIFKSPERTKQFIVY 85

RESULT 3

ID 08NEK6 PRELIMINARY; PRT; 268 AA.
 AC 08NEK6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Prolin-rich Gla (G-carboxyglutamic acid) polypeptide 1
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strauberg R.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030786; AAH30786.1; -.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR00294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00011; GLUT_CARBOXYLATION; 1.
 FT NON_TER
 SQ SEQUENCE 268 AA; 30295 MW; C3A47C2D90007739 CRC64;

Query Match 55.3%; Score 105; DB 4; Length 268;
 Best Local Similarity 43.2%; Pred. No. 3.1e-11;
 Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRXCKXQCSFXAXRIFKDXARTLFWISY 44
 Db 71 ANGFPEIRQNIIECKEKEQCSFEAREIFKSPERTKQFIVY 114

RESULT 4

ID 08K3U6 PRELIMINARY; PRT; 446 AA.
 AC 08K3U6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Coagulation factor VII.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Murphy K., Ramaker M.;
 RT "Nucleotide sequence of the cDNA encoding rat coagulation factor VII.";

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      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR  EMBL; AF532184; AAM95967.1; -.
DR  InterPro; IPR002086; Aldehyde_dehydr.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR003114; Chymotrypsin.
DR  InterPro; IPR000742; EGF_2.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR001438; EGF_II.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR002383; GLA_blood.
DR  InterPro; IPR006210; IEGF.
DR  InterPro; IPR001254; Ser_protease_Try.
DR  InterPro; IPR000294; VltK_dep_GLA.
DR  Pfam; PF00008; EGF_1.
DR  Pfam; PF00594; gla; 1.
DR  Pfam; PF00089; trypsin; 1.
DR  PRINTS; PR00722; CHYMOTRYPSIN.
DR  PRINTS; PR00010; EGFBL00D.
DR  PRINTS; PR00001; GLABLOOD.
DR  SMART; SM00179; EGF_CA; 1.
DR  SMART; SM0069; GLA; 1.
DR  SMART; SM00020; Tryp_Spc; 1.
DR  PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR  PROSITE; PS00010; ASX_HYDROXYL; 1.
DR  PROSITE; PS00022; EGF_1; 1.
DR  PROSITE; PS01187; EGF_CA; 1.
DR  PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR  PROSITE; PS50240; TRYPSIN_DOM; 1.
DR  PROSITE; PS00134; TRYPSIN_HIS; 1.
DR  PROSITE; PS00135; TRYPSIN_SER; 1.
KM  EGF-like domain; Hydrolase; Protease; Serine protease.
SQ  SEQUENCE 446 AA; 50399 MW; 292985EBF119C0AA CRC64;

Query Match          55.3%; Score 105; DB 11; Length 446;
Best Local Similarity 50.0%; Pred. No. 5.2e-11;
Matches 22; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy  1 ANAFLLXLRQSGSLKRXCKXKOCSPFXKXRXIFPDAXRTLFWISY 44
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db  42 ANSLLEELMSSSLRECNERCSCFEAREIFKSPERTKQFWITY 85

RESULT 5
ID  Q8JHC9          PRELIMINARY;      PRT;      443 AA.
AC  Q8JHC9;
DT  01-OCT-2002 (TREMBLrel. 22, Created)
DT  01-OCT-2002 (TREMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Coagulation factor VII.
OS  Brachydanio rerio (Zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxID=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Hanumethaiah R.; Day K.; Jagadeeswaran P.;
RT  "Comprehensive analysis of blood coagulation pathways in Zebrafish:
RT  Evolution of coagulation factor genes and identification of zebrafish
RT  factor VIII."
RL  Blood Cells Mol. Dis. 0:0-0(2002).
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR  EMBL; AF515269; AAN71000.1; -.
DR  InterPro; IPR001314; Chymotrypsin.
DR  InterPro; IPR000742; EGF_2.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR002383; GLA_blood.
DR  InterPro; IPR006210; IEGF.
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DR  InterPro; IPR001254; Ser_protease_Try.
DR  InterPro; IPR000294; VltK_dep_GLA.
DR  Pfam; PF00008; EGF_1.
DR  Pfam; PF00594; gla; 1.
DR  Pfam; PF00089; trypsin; 1.
DR  PRINTS; PR00722; CHYMOTRYPSIN.
DR  PRINTS; PR00001; GLABLOOD.
DR  SMART; SM00181; EGF_2.
DR  SMART; SM00179; EGF_CA; 1.
DR  SMART; SM0069; GLA; 1.
DR  SMART; SM00020; Tryp_Spc; 1.
DR  PROSITE; PS00022; EGF_1; 1.
DR  PROSITE; PS01186; EGF_2; 2.
DR  PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR  PROSITE; PS50240; TRYPSIN_DOM; 1.
DR  PROSITE; PS00134; TRYPSIN_HIS; 1.
KW  EGF-like domain; Hydrolase; Protease; Serine protease.
SQ  SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FP4 CRC64;

Query Match          53.7%; Score 102; DB 13; Length 443;
Best Local Similarity 41.9%; Pred. No. 1.9e-10;
Matches 18; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy  2 NAFLXLRQSGSLKRXCKXKOCSPFXKXRXIFPDAXRTLFWISY 44
    |||::|||::|||::|||::|||::|||::|||::|||::|||
Db  40 SGFLSEKAKGNLRECEVCBEICDYEARREVFDSDRTKQFWISY 82

RESULT 6
ID  Q91WN8          PRELIMINARY;      PRT;      460 AA.
AC  Q91WN8;
DT  01-DEC-2001 (TREMBLrel. 19, Created)
DT  01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT  01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE  Similar to protein C.
DE  PROC.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Strauberg R.;
RT  TISSUE=Liver;
RT  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC  -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR  EMBL; BC013896; AAI13896.1; -.
DR  HSSP; P00761; LAN1.
DR  MED; MGI:97771; Proc.
DR  InterPro; IPR000152; Asx_hydroxyl.
DR  InterPro; IPR001314; Chymotrypsin.
DR  InterPro; IPR001881; EGF_Ca.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR002383; GLA_blood.
DR  InterPro; IPR001254; Ser_protease_Try.
DR  InterPro; IPR000294; VltK_dep_GLA.
DR  Pfam; PF00008; EGF_1.
DR  Pfam; PF00594; gla; 1.
DR  Pfam; PF00089; trypsin; 1.
DR  PRINTS; PR00722; CHYMOTRYPSIN.
DR  PRINTS; PR00001; GLABLOOD.
DR  SMART; SM00179; EGF_CA; 1.
DR  SMART; SM0069; GLA; 1.
DR  SMART; SM00020; Tryp_Spc; 1.
DR  PROSITE; PS00010; ASX_HYDROXYL; 1.
DR  PROSITE; PS00022; EGF_1; 1.
DR  PROSITE; PS01186; EGF_2; 2.
DR  PROSITE; PS01187; EGF_CA; 1.
DR  PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR  PROSITE; PS50240; TRYPSIN_DOM; 1.
DR  PROSITE; PS00134; TRYPSIN_HIS; 1.
DR  PROSITE; PS00135; TRYPSIN_SER; 1.
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DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 50.5%; Score 96; DB 6; Length 469;
Best Local Similarity 38.6%; Pred. No. 2.7e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXARXIFKDXRTKLFWISY 44
Db 41 ANSLFEEFLKKNLERECNEETGYSYEAREVEFDTKNEFWNITY 84

RESULT 10
ID 054740 PRELIMINARY; PRT; 481 AA.
AC 054740;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F10.
OS Mus musculus (Mouse).
OC Plasmid pluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=9845493; PubMed=9783672;
RA Heidmann H.H., Kontermann R.B.;
RT "Cloning and recombinant expression of mouse coagulation factor X";
RU Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AJ222677; CAI0933.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR00438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_blood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.

DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW Plasmid.
FT SIGNAL 41
FT CHAIN 41
SQ SEQUENCE 481 AA; 53986 MW; CF702D5E9FD97AE CRC64;

Query Match 50.5%; Score 96; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 2.8e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXARXIFKDXRTKLFWISY 44
Db 41 ANSFFEEFLKKNLERECMEICSYEAREVEFDDEKTEWYTX 84

RESULT 11
ID 099L32 PRELIMINARY; PRT; 481 AA.
AC 099L32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Coagulation factor X.
GN F10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC003877; AA003877.1; -.
DR HSSP; P00742; 1XKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR00438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR00294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_blood.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW SEQUENCE 481 AA; 54004 MW; BD88B96C8A0B7E7F CRC64;

Query Match 50.5%; Score 96; DB 11; Length 481;
Best Local Similarity 38.6%; Pred. No. 2.8e-09;


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DE Hypothetical protein FLJ90093.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Isegai T., Oca T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Oho T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Minomiyu K.;
RT "NDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK074574; BAC11069.1; -
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR00294; VltK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Hypothetical protein.
SQ SEQUENCE 231 AA; 25944 MW; 8A373B0D5C1D0D81 CRC64;

Query Match 49.5%; Score 94; DB 4; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.1e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQSLRXCKXXQCSFXXRXIFKDXRTKLFWISY 44
Db 20 ANEFLLELRQGTIERECMEICSYEVKVEVENKEMEFWKGY 63

RESULT 15
Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matie U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AJ001979; CAA05126.1; -
DR HSP: P04070; IAT.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.

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DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolyase; Protease; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192
FT CHAIN 193 194
FT CHAIN 195 456
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 48.9%; Score 93; DB 6; Length 456;
Best Local Similarity 40.9%; Pred. No. 9.5e-09;
Matches 18; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANAFLLXLRQSLRXCKXXQCSFXXRXIFKDXRTKLFWISY 44
Db 43 ANSFLLELRQSLRXCKXXQCSFXXRXIFKDXRTKLFWISY 86

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Search completed: July 28, 2003, 12:27:33
 Job time : 61 secs

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XX WPI; 1999-288309/24.
DR Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
PT
XX
PS Disclosure; Page 80; 86pp; English.
XX
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 87.9%; Score 167; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 2.5e-21;
Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXAXRIFKDXRRTKLFWISY 44
Db 1 ANAFLXXLRGSLRXCKXQCSFXAXRIFKDXRRTKLFWISY 44

RESULT 2
AAV18302
ID AAV18302 standard; peptide; 44 AA.
XX
XX AAV18302;
AC
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..44
FT "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
PI
XX
XX W09920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Nelaeetuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX
XX Claim 11; Page 81; 86pp; English.
XX
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.

CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
XX
SQ Sequence 44 AA;

Query Match 87.4%; Score 166; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 3.8e-21;
Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXAXRIFKDXRRTKLFWISY 44
Db 1 ANAFLXXLRGSLRXCKXQCSFXAXRIFKDXRRTKLFWISY 44

RESULT 3
AAV18311
ID AAV18311 standard; peptide; 44 AA.
XX
XX
XX AAV18311;
AC
XX
DT 17-AUG-1999 (first entry)
XX
DE Modified GLA domain of vitamin K-dependent protein.
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
XX therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..44
FT "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
PI
XX
XX W09920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Nelaeetuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX
XX Disclosure; Page 80; 86pp; English.
XX
CC This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
XX
SQ Sequence 44 AA;

Query Match 86.8%; Score 165; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 5.6e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRGSLRXCKXQCSFXAXRIFKDXRRTKLFWISY 44
Db 1 ANAFLXXLRGSLRXCKXQCSFXAXRIFKDXRRTKLFWISY 44

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3.6
RESULT 4
AA18305
ID AA18305 standard; peptide, 44 AA.
XX
AC AA18305;
XX
DT 17-AUG-1999 (first entry)
XX
DE Human factor VII GLA domain.
XX
KW GLA domain; vitamin K-dependent protein; clotting disorder;
therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX WO9920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22152.
XX
PR 23-OCT-1997; 97US-0955636.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 86.3%; Score 164; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 8.3e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
XX
RESULT 5
AAB36395
ID AAB36395 standard; peptide, 44 AA.
XX
AC AAB36395;
XX
DT 27-FEB-2001 (first entry)
XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;

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KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
OS Homo sapiens.
XX
PN WO200066753-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11416.
XX
PR 29-APR-1999; 99US-0302239.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 2001-007226/01.
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity
XX
PS Disclosure; Page 12; 81pp; English.
XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;
XX
Query Match 86.3%; Score 164; DB 22; Length 44;
Best Local Similarity 97.7%; Pred. No. 8.3e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
XX
RESULT 6
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
AC AAB84870;
XX
DT 31-JUL-2001 (first entry)
XX
DE Mutant blood coagulant factor VII (FVII-31).
XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
-Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

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XX  JP2001061479-A.
XX  13-MAR-2001.
XX  24-AUG-1999; 99JP-0237610.
XX  24-AUG-1999; 99JP-0237610.
XX  (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX  WPI: 2001-310677/33.
XX  N-PSDB; AAH19463.
XX  Mutant of blood coagulant factor VII, used for substitution therapy in
XX  the treatment of hemophilia -
XX  Claim 14; Page 20-21; 29pp; Japanese.
XX  The present invention relates to mutants of blood coagulant factor VII
XX  (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX  sequence is one such mutant FVII: VII-31. The mutants can be used as an
XX  agent for the substitution therapy of haemophilia inhibitor patients.
XX  Sequence 401 AA;

Query Match      86.3%; Score 164; DB 22; Length 401;
Best Local Similarity 75.0%; Pred. No. 8.2e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY  1 ANAFLEXLRQGSIXRXCCKXQCSFXXARXIFKDXARTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 ANAFLELRPGSLERCKEKCQCSFEAREIFXDARTKLFWISY 44

RESULT 7
AAB84871
ID  AAB84871 standard; Protein; 401 AA.
XX
XX  AAB84871;
XX
XX  31-JUL-2001 (first entry)
XX
XX  Mutant blood coagulant factor VII (FVII-39).
XX
XX  Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
XX  mutant; mutein.
XX
XX  Homo sapiens.
XX  Synthetic.
XX
XX  Key Location/Qualifiers
XX  FH Misc-difference 235..239
XX  FT /note= "wild-type Val-Pro-Gly-Thr-Thr substituted by
XX  FT Asp-Arg-Lys-Thr-Leu"
XX  FT Misc-difference 311..317
XX  FT /note= "wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
XX  FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX  PN JP2001061479-A.
XX
XX  13-MAR-2001.
XX
XX  24-AUG-1999; 99JP-0237610.
XX
XX  24-AUG-1999; 99JP-0237610.
XX
XX  (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX  WPI: 2001-310677/33.
XX  N-PSDB; AAH19464.
XX
XX  Mutant of blood coagulant factor VII, used for substitution therapy in
PT

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PT  the treatment of hemophilia -
XX
XX  Claim 16; Page 23-24; 29pp; Japanese.
XX
XX  The present invention relates to mutants of blood coagulant factor VII
XX  (FVII) or activated blood coagulant factor VII (FVIIa). The present
XX  sequence is one such mutant FVII: VII-39. The mutants can be used as an
XX  agent for the substitution therapy of haemophilia inhibitor patients.
XX  Sequence 401 AA;

Query Match      86.3%; Score 164; DB 22; Length 401;
Best Local Similarity 75.0%; Pred. No. 8.2e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY  1 ANAFLEXLRQGSIXRXCCKXQCSFXXARXIFKDXARTKLFWISY 44
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  1 ANAFLELRPGSLERCKEKCQCSFEAREIFXDARTKLFWISY 44

RESULT 8
AAR35764
ID  AAR35764 standard; protein; 406 AA.
XX
XX  AAR35764;
XX
XX  25-MAR-2003 (updated)
XX  24-SEP-1993 (first entry)
XX
XX  Factor VII (VII).
XX
XX  PC; protein C; IX; Factor IX; X; Factor X; PT; prothombin; VII;
XX  Factor VII; CF; chymotrypsinogen; SP; serine protease; binding;
XX  exosite; catalytic activity.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
XX  FH Region 1..152
XX  FT /note= "Factor VII light chain"
XX  FT Region 153..406
XX  FT /note= "Factor VII heavy chain"
XX  FT Peptide 374..388
XX  FT /note= "exosite 1"
XX  FT Peptide 290..310
XX  FT /note= "exosite 2"
XX  FT Peptide 290..310
XX  FT /note= "pref. PC polypeptide; claim 2, page 136"
XX  FT Peptide 374..388
XX  FT /note= "pref. PC polypeptide; claim 2, page 136"
XX  FT Peptide 289..304
XX  FT /note= "pref. PC polypeptide; claim 4, page 137"
XX  FT Peptide 290..304
XX  FT /note= "pref. PC polypeptide; claim 4, page 137"
XX  FT Peptide 245..266
XX  FT /note= "claim 9, page 138-139 describes an antibody
XX  FT that reacts with Factor VII; fragments
XX  FT 289-304, 290-304, 290-310, 374-388 and
XX  FT 400-414 but not with fragment 245-266"
XX
XX  WO9309804-A1.
XX
XX  27-MAY-1993.
XX
XX  18-NOV-1992; 92WO-US10242.
XX
XX  18-NOV-1991; 91US-0793989.
XX
XX  (SCRIP ) SCRIPPS RES INST.
XX  Griffn JH, Masters RM;
XX
XX  WPI: 1993-182244/22.
XX
XX  Mutant of blood coagulant factor VII, used for substitution therapy in
PT

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XX	Serine protease derived-polypeptide(s) and anti-peptide antibodies - for inhibiting coagulation and assaying for the presence of serine protease in fluid samples
PT	Disclosure; Page 133-135; 149pp; English.
PS	
XX	
CC	The PC polypeptides indicated in the Features Table inhibit coagulation (they prevent binding of serine protease to natural substrates), esp. when admin. to give an intravascular blood concn. of 0.1-100 (pref. 0.5-10) microm.
CC	NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described in the specification but have not yet been added to the SEQUENCE LISTING.
CC	(Updated on 25-MAR-2003 to correct PN field.)
CC	
XX	
SQ	Sequence 406 AA;
Query Match	86.3%; Score 164; DB 14; Length 406;
Best Local Similarity	75.0%; Pred. No. 8.3e-20;
Matches 33; Conservative	0; Mismatches 11; Indels 0; Gaps 0;
Oy	1 AANAFLXXLRGGSLKRXCKXCCGCFXAXIFPDAXRTLFWISY 44 1 ANAFLLELRPSSLRECKEKEQCSEFAAREIRFDABERTLFWISY 44
Dd	
RESULT 9	
AAM14509	
ID	AAM14509 standard; protein; 406 AA.
XX	
AC	AAM14509;
XX	
DT	25-MAR-2003 (updated)
DT	14-MAY-1997 (first entry)
XX	
DE	Modified blood coagulation Factor VII (R290S).
XX	
KW	Blood coagulation; factor 7; mutein; mutation; modification; thrombocytopenia; von Willebrand's disease; plasma substitute.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FH	Location/Qualifiers
FT	6 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	7 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	14 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	16 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	19 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	20 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	26 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	25 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	29 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	29 /label= OTHER
FT	/note= "gamma-carboxylutamic acid"
FT	

FT	Cleavage-site	32..33	/note= "proteolytic site"
FT		35	
FT	Modified-site	/label= "OTHER	
FT		/note= "gamma-carboxyglutamic acid"	
FT		38..39	
FT	Cleavage-site	/note= "proteolytic site"	
FT		42..43	
FT	Cleavage-site	/note= "proteolytic site"	
FT		44..45	
FT		/note= "proteolytic site"	
FT	Disulfide-bond	50..61	
FT	Disulfide-bond	55..70	
FT	Modified-site	63	
FT		/label= OTHER	
FT		/note= "beta-hydroxy-aspartic acid"	
FT		72..81	
FT	Disulfide-bond	91..102	
FT	Disulfide-bond	98..112	
FT	Disulfide-bond	114..127	
FT	Disulfide-bond	135..162	
FT	Cleavage-site	143..144	
FT		/note= "proteolytic site"	
FT	Modified-site	145	
FT		/note= "glycosylation site"	
FT	Disulfide-bond	159..164	
FT	Disulfide-bond	178..194	
FT	Active-site	193	
FT	Active-site	242	
FT	Active-site	344	
FT	Cleavage-site	290..291	
FT		/note= "proteolytic site in unmodified factor VII"	
FT	Misc-difference	290	
FT		/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"	
FT			
FT	Disulfide-bond	310..329	
FT	Cleavage-site	315..316	
FT		/note= "proteolytic site"	
FT	Modified-site	322	
FT		/note= "glycosylation site"	
FT	Disulfide-bond	340..368	
FT	Cleavage-site	341..342	
FT		/note= "proteolytic site"	
FT	Cleavage-site	392..393	
FT		/note= "proteolytic site"	
FT	Cleavage-site	396..397	
FT		/note= "proteolytic site"	
FT	Cleavage-site	402..403	
FT		/note= "proteolytic site"	
PN	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	22-AUG-1994;	94US-0293778.	
XX			
PR	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898228.	
PR	22-AUG-1994;	94US-0293778.	
XX			
PA	(NOVO) NOVO-NORDISK AS.		
XX			
PI	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX			
DR	WPI; 1997-035523/03.		
XX			
PT	Mutated human factor VII or VIIa proteins - with amino acid		
PT	substitutions to improve proteolytic stability		
XX			
PS	Example 3; Page -; 28pp; English.		
XX			

CC Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
 CC bleeding disorders such as thrombocytopenia and von Willebrand's
 CC disease. They are also suitable for addition to plasma substitutes.
 CC The present sequence is a specific example of a modified factor VII
 CC protein.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX
 SQ Sequence 406 AA:
 Query Match 86.3%; Score 164; DB 18; Length 406;
 Best Local Similarity 75.0%; Pred. No. 8.3e-20;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 Oy 1 ANAFLLXLRQGSLLRXKXKXQGSFYXARXIFDAXRTKLFWISY 44
 1 ANAFLELRPGSLRECKEKGCSFEAREIFDARERTKLFWISY 44
 Db
 RESULT 10
 AAW14510
 ID AAW14510 standard; protein; 406 AA.
 XX
 AC AAW14510;
 XX
 XX 25-MAR-2003 (updated)
 DT 14-MAY-1997 (first entry)
 XX
 DE Modified blood coagulation Factor VII (R315S).
 XX
 KW Blood coagulation; factor 7; mutain; mutation; modification;
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 6 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 7 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 14 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 16 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 19 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 20 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Disulfide-bond 17..22 /note= "gamma-carboxyglutamic acid"
 FT Modified-site 25 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 26 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Modified-site 29 /label= OTHER
 FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 32..33 /note= "gamma-carboxyglutamic acid"
 FT Modified-site 35 /label= OTHER
 FT /label= OTHER

FT /note= "gamma-carboxyglutamic acid"
 FT Cleavage-site 38..39 /note= "proteolytic site"
 FT Cleavage-site 42..43 /note= "proteolytic site"
 FT Cleavage-site 44..45 /note= "proteolytic site"
 FT Disulfide-bond 50..61 /note= "proteolytic site"
 FT Disulfide-bond 55..70 /label= OTHER
 FT Modified-site 63 /label= "beta-hydroxy-aspartic acid"
 FT Disulfide-bond 72..81 /note= "proteolytic site"
 FT Disulfide-bond 91..102 /note= "proteolytic site"
 FT Disulfide-bond 98..112 /note= "proteolytic site"
 FT Disulfide-bond 114..127 /note= "proteolytic site"
 FT Disulfide-bond 135..162 /note= "proteolytic site"
 FT Cleavage-site 143..144 /note= "proteolytic site"
 FT Modified-site 145 /note= "glycosylation site"
 FT Disulfide-bond 159..164 /note= "glycosylation site"
 FT Disulfide-bond 178..194 /note= "glycosylation site"
 FT Active-site 193 /note= "glycosylation site"
 FT Active-site 242 /note= "glycosylation site"
 FT Active-site 344 /note= "glycosylation site"
 FT Cleavage-site 290..291 /note= "proteolytic site"
 FT Disulfide-bond 310..329 /note= "proteolytic site"
 FT Cleavage-site 315..316 /note= "proteolytic site"
 FT Misc-difference 315 /note= "proteolytic site in unmodified factor VII"
 FT /note= "native Arg315 has been substituted by Ser to
 FT provide a proteolytically more stable peptide
 FT bond"
 FT Modified-site 322 /note= "glycosylation site"
 FT Disulfide-bond 340..368 /note= "glycosylation site"
 FT Cleavage-site 341..342 /note= "proteolytic site"
 FT Cleavage-site 392..393 /note= "proteolytic site"
 FT Cleavage-site 396..397 /note= "proteolytic site"
 FT Cleavage-site 402..403 /note= "proteolytic site"
 FT /note= "proteolytic site"
 XX
 XX US5580560-A.
 PN
 XX
 XX 03-DEC-1996.
 PD
 XX
 XX 22-AUG-1994; 94US-0293778.
 PF
 XX 09-AUG-1993; 93US-0104509.
 PR 13-NOV-1989; 89US-0434149.
 PR 12-JUN-1992; 92US-0898248.
 PR 22-AUG-1994; 94US-0293778.
 XX
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;
 PI WPI; 1997-033523/03.
 XX
 XX Mutated human factor VII or VIIa proteins - with amino acid
 FT substitutions to improve proteolytic stability
 FT
 XX Example 4; Page -; 28pp; English.
 PS
 XX Modified human factor VII or VIIa proteins are stabilised against
 CC proteolytic cleavage by substitution of one of the residues Lys32,
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and
 CC Lys341 by an amino acid that provides a proteolytically more stable

CC peptide bond, provided that Lys32 is replaced by Glu, Glu, His,
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating
CC bleeding disorders such as thrombocytopenia and von Willebrand's
CC disease. They are also suitable for addition to plasma substitutes.
CC The present sequence is a specific example of a modified factor VII
CC protein.
CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 406 AA;

Query Match 86.3%; Score 164; DB 18; Length 406;
Best Local Similarity 75.0%; Pred. No. 8.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCXKXCSFYXARXIFKDAKFTKLFWISY 44
Db 1 ANAFLELRPGSLRBECKECSEFEAREIKDAERTKLFWISY 44

RESULT 11
AAU77745
ID AAU77745 standard; protein; 406 AA.

AC AAU77745;

DT 05-JUN-2002 (first entry)

DE Human factor VIIa active site mutant.

KM Factor VIIa; human; shock heat treatment; protein stability;
KW protein manufacture; protein conformation; mutant; mutain.

XX Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers

FT Active-site 193

FT Active-site /note= "Member of the factor VIIa catalytic triad"

FT Active-site 242

FT Active-site /note= "Member of the factor VIIa catalytic triad"

FT Active-site 344

FT Misc-difference /note= "Member of the factor VIIa catalytic triad"

FT /label= Gly, Met, Thr

FT /note= "Preferably Ala. Wild type Ser"

PN W0200177141-A1.

PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-DK0234.

PR 06-APR-2000; 2000DK-0000573.

PR 17-APR-2000; 2000US-197650P.

PA (NOVO) NOVO NORDISK AS.

PI Mathiesen F;

DR WPI; 2001-657162/75.

PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition

PT involves a shock heat treatment

PS Disclosure; Page -; 22pp; English.

CC The invention describes a method of stabilising a polypeptide involving
CC shock heat treatment of the polypeptide. The method is useful in a
CC pharmaceutical composition, in the industrial or large scale method of
CC manufacturing a polypeptide, also as a unit operation during preparation,
CC purification, recovery and/or formulation of polypeptides. The shock heat
CC treatment improves the protein stability without substantial loss of
CC biological activity. The method can be applied to change polypeptide

CC conformation in a very fast and non-invasive manner. The polypeptide
CC formed is stable. The method is also useful for decreasing the
CC association of the polypeptide. This sequence represents a modified
CC human factor VIIa protein, mutated at the catalytic site, described
CC in the invention.
CC Note: This sequence does not appear in the specification but has
CC been obtained using information given in the invention.

SQ Sequence 406 AA;

Query Match 86.3%; Score 164; DB 22; Length 406;
Best Local Similarity 75.0%; Pred. No. 8.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCXKXCSFYXARXIFKDAKFTKLFWISY 44
Db 1 ANAFLELRPGSLRBECKECSEFEAREIKDAERTKLFWISY 44

RESULT 12
AAM52171
ID AAM52171 standard; Protein; 406 AA.

AC AAM52171;

DT 07-FEB-2002 (first entry)

DE Human FVII SEQ ID NO 1.

XX Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
KW cardiatic; hepatocytic; cerebroprotective; haemophilia; liver disease;
KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.

XX Homo sapiens.
OS

FH Key Location/Qualifiers

FT Misc-difference 6

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 7

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 14

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 16

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 19

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 20

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 25

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 26

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 29

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Misc-difference 35

FT /label= Glu, OTHER

FT /note= "OTHER = gamma carboxylutamic acid"

FT Modified-site 52

FT /note= "O-glycosylated"

FT Modified-site 60

FT /note= "O-glycosylated"

FT Modified-site 145

FT /note= "N-glycosylated"

FT Cleavage-site 152..153

FT	/note= "proteolytic cleavage site converting FVII zymogen
FT	to an activated form, comprising two chains
FT	linked by a single disulphide bridge"
FT	Modified-site 322 /note= "N-glycosylated"
XX	
PN	WO200156935-A2.
XX	
PD	16-AUG-2001.
XX	
PF	12-FEB-2001; 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAXY-) MAXYGEN APS.
XX	
PJ	Anderseen KV, Pedersen AH, Bornaaes C;
XX	
DR	WPI; 2001-581807/65.
DR	N-PESDB; AA199982.
XX	
PT	New conjugate, useful for treating Factor VIIA related diseases or
PT	disorders such as haemophilia, liver disease, myocardial infarction and
PT	deep-vein thrombosis), comprises non-polypeptide group covalently
PT	attached to polypeptide group -
XX	
PS	Claim 1, Page 81-83; 8ppp; English.
XX	
CC	The invention relates to novel Factor VII (FVII) or Factor VIIA (FVIIa)
CC	polypeptide conjugates, comprising at least one non-polypeptide group
CC	covalently attached to a polypeptide, where the amino acid sequence of
CC	polypeptide differs from that of the wildtype FVIIA (AAM52171) in that at
CC	least one amino acid residue containing an attachment group for the
CC	non-polypeptide group has been introduced or removed. The FVIIa
CC	conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
CC	cerebroprotective activity and are useful for treating FVIIa/VF-related
CC	diseases or disorders such as haemophilia, liver disease, myocardial
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC	have increased functional in vivo half life and/or increased plasma half
CC	life, increased bioavailability and or reduced sensitivity to proteolytic
CC	degradation. Consequently medical treatment using the conjugates has a
CC	number of advantages over currently available such as longer duration
CC	between injections.
CC	
SQ	Sequence 406 AA;
Query Match	86.3%; Score 164; DB 22; Length 406;
Best Local Similarity	97.7%; Pred.No. 8.3e-20;
Matches 43; Conservative	0; Mismatches 1; Indels 0; Gaps 0
Oy	1 ANAFPLXLRQSGSLRXRCCKXQCSPFXARXIFPDARTKLFWISY 44
Ddb	1 ANAFPLXLRPGSLRXRCCKXCXGSPFXARXIFPDARTKLFWISY 44
RESULT 13	
AAM52172	
ID	AAM52172 standard; Protein; 406 AA.
XX	
AC	AAM52172;
XX	
DT	07-FEB-2002 (first entry)
DE	
XX	Mammalian expressed human FVII SEQ ID NO 3.
XX	
KW	Factor VII; FVII; Factor VIIA; FVIIa; haemostatic; thrombolytic;
KW	cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis.
OS	Homo sapiens.
PH	
Key .	Location/Qualifiers

FT	Modified-site	52	/note= "O-glycosylated"
FT	Modified-site	60	/note= "O-glycosylated"
FT	Modified-site	145	/note= "N-glycosylated"
FT	Cleavage-site	152..153	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Modified-site	322	/note= "N-glycosylated"
PN	WO200158935-A2.		
XX	16-AUG-2001.		
PD			
XX	12-FEB-2001; 2001WO-DK00094.		
PF			
XX	11-FEB-2000; 2000DK-0000218.		
PR	18-OCT-2000; 2000DK-0001558.		
XX	(MAXY-) MAXGEN APS.		
PA			
XX	Anderesen KV, Pedersen AH, Bornaes C;		
PI			
XX	WPI, 2001-581807/65.		
DR	N-PGDB; AA199983.		
XX	New conjugate, useful for treating Factor VIIa related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -		
PT			
XX	Disclosure: Page 85-86; 89pp; English.		
PS			
XX	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)		
CC	polypeptide conjugates, comprising at least one non-polypeptide group		
CC	covalently attached to a polypeptide, where the amino acid sequence of		
CC	polypeptide differs from that of the wildtype FVIIa (AAM52181) in that at		
CC	least one amino acid residue containing an attachment group for the		
CC	non-polypeptide group has been introduced or removed. The FVIIa		
CC	conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and		
CC	cardioprotective activity and are useful for treating FVIIa/TF-related		
CC	diseases or disorders such as haemophilia, liver disease, myocardial		
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates		
CC	have increased bioavailability and/or reduced sensitivity to proteolytic		
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic		
CC	degradation. Consequently medical treatment using the conjugates has a		
CC	number of advantages over currently available such as longer duration		
CC	between injections.		
XX			
XX			
SQ	Sequence 406 AA;		
Query Match	86.3%; Score 164; DB 22; Length 406;		
Best Local Similarity	75.0%; Pred. No. 8.3e-20;		
Matches 33; Conservative	0; Mismatches 11; Indels 0; Gaps 0;		
Oy	1 ANAFIXLRQSLRXCKXCCSPFXRXRIFKDAXRTLGFWSY 44 		
Db	1 ANAFLERLPGSLERECKEBCSCFEARIRKDARTLFWISY 44 		
RESULT 14			
AAM52181			
ID	AAM52181 standard; Protein; 406 AA.		
XX			
AC	AAM52181;		
XX			
DT	07-FEB-2002 (First entry)		
XX			
DE	Human FVII mutant T106N.		
XX			

KM Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KM cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KM murein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 6
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 7
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 14
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
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 FT Misc-difference 19
 FT /label= Glu, OTHER
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 FT Misc-difference 20
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 FT Misc-difference 25
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 FT Misc-difference 26
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 FT Misc-difference 29
 FT /label= Glu, OTHER
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 FT Misc-difference 35
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 FT /note= "OTHER = gamma carboxyglutamic acid"
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 FT Modified-site 60
 FT /note= "O-glycosylated"
 FT Misc-difference 106
 FT /note= "O-glycosylated"
 FT Modified-site 145
 FT /note= "Wild-type Thr substituted by Asn"
 FT Cleavage-site 152..153
 FT /note= "proteolytic cleavage site converting FVII zymogen
 FT to an activated form, comprising two chains
 FT linked by a single disulphide bridge"
 FT Modified-site 322
 FT /note= "N-glycosylated"
 FT
 XX WO200158935-A2.
 PN 16-AUG-2001.
 PD
 XX 12-FEB-2001; 2001WO-DK00094.
 PF
 XX 11-FEB-2000; 2000DK-0000218.
 PR 18-OCT-2000; 2000DK-0001558.
 XX
 PA (MAXY-) MAXYGEN APS.
 XX
 PI Andersen KV, Pedersen AH, Bornaes C;
 XX
 DR WPI; 2001-581807/65.
 XX
 PT New conjugate, useful for treating Factor VIIa related diseases or
 PT disorders such as haemophilia, liver disease, myocardial infarction and
 PT deep-vein thrombosis, comprises non-polypeptide group covalently
 PT attached to polypeptide group -

XX Example 3; Page -: 89pp; English.
 PS
 XX The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
 CC polypeptide conjugates, comprising at least one non-polypeptide group
 CC covalently attached to a polypeptide, where the amino acid sequence of
 CC polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
 CC least one amino acid residue containing an attachment group for the
 CC non-polypeptide group has been introduced or removed. The FVIIa
 CC conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
 CC cerebroprotective activity and are useful for treating FVIIa/TF-related
 CC diseases or disorders such as haemophilia, liver disease, myocardial
 CC infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
 CC have increased functional in vivo half life and/or increased plasma half
 CC life, increased bioavailability and/or reduced sensitivity to proteolytic
 CC degradation. Consequently medical treatment using the conjugates has a
 CC number of advantages over currently available such as longer duration
 CC between injections. The present sequence is that of a human FVII mutant,
 CC having an addition in vivo glycosylation site and tested for its
 CC amidolytic activity.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the human wild-type FVII sequence shown in SEQ ID NO 1
 CC (AAM52171).
 XX
 SQ Sequence 406 AA;
 Query Match 86.3%; Score 164; DB 22; Length 406;
 Best Local Similarity 97.7%; Pred. No. 8.3e-20;
 Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 ANAFLLXLRQSLXRXCKXQCSFXRXRXIFDXARTKLFWISY 44
 Db 1 ANAFLLXLRQSLXRXCKXQCSFXRXRXIFDXARTKLFWISY 44
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 AAM52182
 ID AAM52182 standard; Protein: 406 AA.
 AC
 XX AAM52182;
 DT
 XX 07-FEB-2002 (first entry)
 DE Human FVII mutant K143N/N145T.
 XX
 XX Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
 KM cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
 KM myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
 KM murein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 6
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 7
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 14
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
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 FT /label= Glu, OTHER
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 FT Misc-difference 19
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 20
 FT /label= Glu, OTHER
 FT /note= "OTHER = gamma carboxyglutamic acid"
 FT Misc-difference 25
 FT /note= "OTHER = gamma carboxyglutamic acid"

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FT	/note= "OTHER = gamma carboxyglutamic acid"	
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FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	29	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	35	
FT	/label= Glu, OTHER	
FT	/note= "OTHER = gamma carboxyglutamic acid"	
FT	52	
FT	/note= "O-glycosylated"	
FT	60	
FT	/note= "O-glycosylated"	
FT	143	
FT	/note= "O-glycosylated"	
FT	145	
FT	/note= "Wild-type Lys substituted by Asn"	
FT	152, 153	
FT	/note= "Wild-type Asn substituted by Thr"	
FT	/note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"	
FT	322	
FT	/note= "N-glycosylated"	
XX		
PN	WO200158935-A2.	
XX		
PD	16-AUG-2001.	
XX		
PF	12-FEB-2001; 2001WO-DK00094.	
XX		
PR	11-FEB-2000; 2000DK-0000218.	
XX	18-OCT-2000; 2000DK-0001558.	
XX		
PA	(MAXY-) MAXYGEN APS.	
PI	Anderseen KV, Pedersen AH, Bornhaes C;	
DR	WPI; 2001-581807/65.	
XX		
PT	New conjugate, useful for treating Factor VIIA related diseases or disorders such as haemophilia, liver disease, myocardial infarction and deep-vein thrombosis, comprises non-polypeptide group covalently attached to polypeptide group -	
XX		
PS	Example 3; Page -; 89pp; English.	
XX		
CC	The invention relates to novel Factor VII (FVII) or Factor VIIA (FVIIa) polypeptide conjugates, comprising at least one non-polypeptide group covalently attached to a polypeptide, where the amino acid sequence of polypeptide differs from that of the wildtype FVIIA (AAM52171) in that at least one amino acid residue containing an attachment group for the non-polypeptide group has been introduced or removed. The FVIIa conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and cerebroprotective activity and are useful for treating FVIIa/TF-related diseases or disorders such as haemophilia, liver disease, myocardial infarction, thrombotic stroke and deep-vein thrombosis. The conjugates have increased functional in vivo half life and/or increased plasma half life, increased bioavailability and or reduced sensitivity to proteolytic degradation. Consequently medical treatment using the conjugates has a number of advantages over currently available such as longer duration between injections. The present sequence is that of a human FVII mutant, having an addition in vivo glycosylation site and tested for its amidolytic activity.	
CC	Note: The present sequence is not shown in the specification but is derived from the human wild-type FVII sequence shown in SEQ ID NO 1 (AAM52171).	
XX		
XX	Sequence 406 AA;	

	Matches	43;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
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Db	1	ANAFXXLRPGSLRXCCXXQCSFXAXRXIFKDA	RTKLFWISY	44						

Search completed: July 28, 2003, 12:23:52
Job time : 37 secs

Query Match	86.3%;	Score 164;	DB 22;	Length 406;
Best Local Similarity	97.7%;	Pred. No. 8.3e-20;		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:25:31 ; Search time 32.5 Seconds
(without alignments)
160.782 Million cell updates/sec

Title: SEQ3
Perfect score: 190
Sequence: 1 ANAFLLXLRGSLRXCKXKX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BIOSIM62
Gap 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	86.3	44	US-10-298-330-3	Sequence 3, Appl1
2	164	86.3	406	US-09-782-587B-1	Sequence 1, Appl1
3	164	86.3	406	US-09-782-587B-3	Sequence 3, Appl1
4	164	86.3	406	US-10-109-498-1	Sequence 1, Appl1
5	164	86.3	406	US-10-255-032-1	Sequence 1, Appl1
6	164	86.3	406	US-10-281-727-1	Sequence 1, Appl1
7	164	86.3	466	US-10-017-122-2	Sequence 2, Appl1
8	144	75.8	40	US-10-298-330-23	Sequence 23, Appl1
9	138	72.6	40	US-10-298-330-22	Sequence 22, Appl1
10	138	72.6	40	US-10-298-330-25	Sequence 25, Appl1
11	137	72.1	40	US-10-298-330-26	Sequence 26, Appl1
12	132	69.5	40	US-10-298-330-24	Sequence 24, Appl1
13	123	64.7	44	US-10-298-330-4	Sequence 4, Appl1
14	114.5	60.3	41	US-10-298-330-27	Sequence 27, Appl1
15	107	56.3	44	US-10-298-330-18	Sequence 18, Appl1

16	102	53.7	419	US-10-182-263-6	Sequence 6, Appl1
17	97	51.1	419	US-10-182-263-3	Sequence 3, Appl1
18	97	51.1	419	US-10-182-263-4	Sequence 4, Appl1
19	97	51.1	419	US-10-182-263-5	Sequence 5, Appl1
20	96	50.5	44	US-10-298-330-2	Sequence 2, Appl1
21	95	50.0	426	US-09-951-121A-1	Sequence 1, Appl1
22	95	50.0	426	US-10-295-682-1	Sequence 1, Appl1
23	88	46.3	45	US-10-298-330-5	Sequence 5, Appl1
24	88	46.3	415	US-09-118-748-2	Sequence 2, Appl1
25	88	46.3	461	US-09-684-901-3	Sequence 3, Appl1
26	88	46.3	461	US-10-132-829-5	Sequence 5, Appl1
27	88	46.3	461	US-10-234-406-6	Sequence 6, Appl1
28	88	46.3	461	US-10-234-406-8	Sequence 8, Appl1
29	86	45.3	44	US-10-298-330-1	Sequence 1, Appl1
30	86	45.3	419	US-09-978-917A-4	Sequence 4, Appl1
31	86	45.3	419	US-10-182-263-1	Sequence 1, Appl1
32	86	45.3	461	US-09-978-917A-2	Sequence 2, Appl1
33	86	45.3	461	US-10-182-263-2	Sequence 2, Appl1
34	85	44.7	622	US-10-020-141-8	Sequence 8, Appl1
35	85	44.7	622	US-10-017-631-2	Sequence 2, Appl1
36	85	44.7	622	US-10-214-932-116	Sequence 116, App
37	85	44.7	622	US-10-172-712-29	Sequence 29, Appl1
38	77.5	40.8	46	US-10-298-330-6	Sequence 6, Appl1
39	74.5	39.2	96	US-09-759-130B-313	Sequence 313, App
40	74.5	39.2	11	US-10-189-123-43	Sequence 43, Appl1
41	74.5	39.2	209	US-09-759-130B-312	Sequence 312, App
42	74.5	39.2	209	US-10-189-123-42	Sequence 42, Appl1
43	74.5	39.2	226	US-09-759-130B-310	Sequence 310, App
44	74.5	39.2	226	US-10-189-123-40	Sequence 40, Appl1
45	67	35.3	44	US-10-298-330-19	Sequence 19, Appl1

ALIGNMENTS

RESULT 1
US-10-298-330-3
: Publication 3, Application US/10298330
: Publication No. US20030100506A1
: GENERAL INFORMATION:
: APPLICANT: Neisestuen, Gary L.
: TITLE OF INVENTION: Modified Vitamin K-Dependent
: FILE REFERENCE: 09531-127001
: CURRENT APPLICATION NUMBER: US/10/298,330
: CURRENT FILING DATE: 2002-11-18
: PRIOR APPLICATION NUMBER: 09/497,591
: PRIOR FILING DATE: 2000-02-03
: PRIOR APPLICATION NUMBER: 09/302,239
: PRIOR FILING DATE: 1999-04-29
: PRIOR APPLICATION NUMBER: 08/955,636
: PRIOR FILING DATE: 1997-10-23
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURES:
: NAME/KEY: VARIANT
: LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
: OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-3

Query Match 86.3%; Score 164; DB 15; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.1e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
Db 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44

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RESULT 2
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (16)
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; LOCATION: (19)..(20)
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; NAME/KEY: MOD RES
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1
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Best Local Similarity 97.7%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANAFLLXLRQSLRXCKXXQCSFXXARXIFKDXARTLFWISY 44
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US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
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; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3
Query Match      86.3%; Score 164; DB 11; Length 406;
Best Local Similarity 75.0%; Pred. No. 1e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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RESULT 4
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286,200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1
Query Match      86.3%; Score 164; DB 15; Length 406;
Best Local Similarity 97.7%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ANAFLLXLRQSLRXCKXXQCSFXXARXIFKDXARTLFWISY 44
DB      1 ANAFLLXLRPGSLRXCKXXQCSFXXARXIFKDXARTLFWISY 44

RESULT 5
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A1O No. US20030100075A1disk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation factor VII
; FEATURE:
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NAME/KEY: MISC FEATURE
LOCATION: (1)..(406)
OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-255-032-1
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Query Match      86.3%; Score 164; DB 15; Length 406;
Best Local Similarity 97.7%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      1 ANAFLLXLRQSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
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RESULT 6
US-10-281-727-1
Sequence 1, Application US/10281727
Publication No. US2003013019A1
GENERAL INFORMATION:
APPLICANT: Persson, Bgon
APPLICANT: Olsson, Ole Hvilsted
TITLE OF INVENTION: Human Coagulation Factor VII
FILE REFERENCE: 6410.200-US
CURRENT APPLICATION NUMBER: US/10/281.727
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PA 2001 01627
PRIOR FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/335,383
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 406
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
US-10-281-727-1
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Query Match      86.3%; Score 164; DB 16; Length 406;
Best Local Similarity 97.7%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db      1 ANAFLLXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
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RESULT 7
US-10-017-122-2
Sequence 2, Application US/10017122
Publication No. US2003008724A1
GENERAL INFORMATION:
APPLICANT: McGarity, Jeanette
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
FILE REFERENCE: MMI-007
CURRENT APPLICATION NUMBER: US/10/017.122
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/327,487
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 466
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-122-2
```

```
Query Match      86.3%; Score 164; DB 15; Length 466;
Best Local Similarity 75.0%; Pred. No. 1.2e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
OY      1 ANAFLLXLRQSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
Db      61 ANAFLELRPGSLRECKEKCSEFARARIFKDXRTKLFWISY 104
```

```
RESULT 8
US-10-298-330-23
Sequence 23, Application US/10298330
Publication No. US20030100506A1
GENERAL INFORMATION:
APPLICANT: Neleestuen, Gary L.
TITLE OF INVENTION: Modified Vitamin K-Dependent
FILE REFERENCE: 09531-127001
CURRENT APPLICATION NUMBER: US/10/298.330
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/497,591
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/302,239
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-23
```

```
Query Match      75.8%; Score 144; DB 15; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.3e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ANAFLLXLRQSLRXCKXQCSFXXARXIFKDXRTKLF 40
Db      1 ANAFLLXLRQSLRXCKXQCSFXXARXIFKDXRTKLF 40
```

```
RESULT 9
US-10-298-330-22
Sequence 22, Application US/10298330
Publication No. US20030100506A1
GENERAL INFORMATION:
APPLICANT: Neleestuen, Gary L.
TITLE OF INVENTION: Modified Vitamin K-Dependent
FILE REFERENCE: 09531-127001
CURRENT APPLICATION NUMBER: US/10/298.330
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/497,591
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/302,239
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 40
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD RES
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-22
```

Query Match 72.6%; Score 138; DB 15; Length 40;
Best Local Similarity 97.5%; Pred. No. 3.8e-17;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40
Db 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40

RESULT 10
US-10-298-330-25

; Sequence 25, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-25

Query Match 72.6%; Score 138; DB 15; Length 40;
Best Local Similarity 97.5%; Pred. No. 3.8e-17;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40
Db 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40

RESULT 11
US-10-298-330-26

; Sequence 26, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 33, 35

; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-26

Query Match 72.1%; Score 137; DB 15; Length 40;
Best Local Similarity 97.5%; Pred. No. 5.7e-17;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40
Db 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40

RESULT 12
US-10-298-330-24

; Sequence 24, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-24

Query Match 69.5%; Score 132; DB 15; Length 40;
Best Local Similarity 95.0%; Pred. No. 4.3e-16;
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40
Db 1 ANAFXXLRQGSIXRXCXKXQCSFXXARXIFKDXARTKLF 40

RESULT 13
US-10-298-330-4

; Sequence 4, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus

```
; FEATURE: 1
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-4
```

```
Query Match
Best Local Similarity 64.7%; Score 123; DB 15; Length 44;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 ANAFLLXLRGSLRXCKXXQCSFXXRXIFKDXRRTKLPWISY 44
Db 1 ANAFLLXLRGSLRXCKXXQCSFXXRXIFRNXXRTROFWVSY 44
```

```
RESULT 14
US-10-298-330-27
```

```
; Sequence 27, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Neissestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
```

```
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
```

```
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
```

```
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
```

```
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 27
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 7, 8, 15, 17, 20, 21, 26, 27, 30, 33, 35, 36
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-27
```

```
Query Match
Best Local Similarity 60.3%; Score 114.5; DB 15; Length 41;
Matches 37; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
```

```
Qy 1 ANA-FLXXLRGSLRXCKXXQCSFXXRXIFKDXRRTKLP 40
Db 1 ANAFLLXLRGSLRXCKXXQCSFXXRXIFRNXXRTKLP 41
```

```
RESULT 15
US-10-298-330-18
```

```
; Sequence 18, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Neissestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
```

```
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
```

```
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
```

```
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
```

```
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
```

```
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35, 39
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-18
```

```
Query Match
Best Local Similarity 56.3%; Score 107; DB 15; Length 44;
Matches 30; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 1 ANAFLLXLRGSLRXCKXXQCSFXXRXIFKDXRRTKLPWISY 44
Db 1 ANAFLLXLRGSLRXCKXXQCSFXXRXIFRNXXRTROFWVSY 44
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Search completed: July 28, 2003, 12:38:59
Job time : 33.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 12:22:40 ; Search time 20 Seconds
(without alignments)
93.084 Million cell updates/sec

Title: SEQ3
Perfect score: 190
Sequence: 1 ANAFLXXLRGSLXRCXKX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	167	87.9	44	3	US-08-955-636-26
2	166	87.4	44	3	US-08-955-636-30
3	165	86.8	44	3	US-08-955-636-27
4	164	86.3	44	3	US-08-955-636-3
5	164	86.3	406	1	US-08-293-778-24
6	164	86.3	406	1	US-08-295-411-5
7	164	86.3	406	2	US-08-955-471-5
8	164	86.3	406	5	PCT-US92-10242-5
9	164	86.3	444	1	US-08-475-845-2
10	164	86.3	444	2	US-08-327-690-2
11	164	86.3	444	2	US-08-660-289-2
12	164	86.3	444	2	US-08-537-807-2
13	164	86.3	444	2	US-08-871-003-2
14	164	86.3	444	3	US-08-464-233-2
15	164	86.3	444	3	US-09-189-607-2
16	164	86.3	444	3	US-09-378-907-2
17	164	86.3	444	5	PCT-US94-05779-2
18	164	86.3	466	1	US-07-882-202A-4
19	164	86.3	466	1	US-08-021-615A-4
20	164	86.3	466	1	US-08-321-777-4
21	164	86.3	466	3	US-09-009-217-14
22	164	86.3	466	3	US-09-009-656-14
23	164	86.3	466	5	PCT-US93-04493-4
24	158	83.2	44	3	US-08-955-636-29
25	156	82.1	44	3	US-08-955-636-28
26	149	78.4	41	1	US-08-229-280-4
27	123	64.7	44	3	US-08-955-636-4

28	113	59.5	139	1	US-08-330-978-2	Sequence 2, Appl
29	113	59.5	139	1	US-08-474-042-2	Sequence 2, Appl
30	113	59.5	139	1	US-08-484-558-2	Sequence 2, Appl
31	113	59.5	139	1	US-08-774-592-2	Sequence 2, Appl
32	113	59.5	437	1	US-08-487-037-2	Sequence 2, Appl
33	113	59.5	437	1	US-08-487-037-3	Sequence 3, Appl
34	113	59.5	488	1	US-08-487-037-1	Sequence 1, Appl
35	107	56.3	44	3	US-08-955-636-18	Sequence 18, Appl
36	107	56.3	487	2	US-08-469-486-53	Sequence 53, Appl
37	107	56.3	487	2	US-08-469-486-53	Sequence 53, Appl
38	107	56.3	492	1	US-08-469-486-2	Sequence 2, Appl
39	107	56.3	492	2	US-08-469-486-2	Sequence 2, Appl
40	104	54.7	448	1	US-08-295-411-3	Sequence 3, Appl
41	104	54.7	448	2	US-08-955-471-3	Sequence 3, Appl
42	104	54.7	448	5	PCT-US92-10068-1	Sequence 1, Appl
43	104	54.7	448	5	PCT-US92-10242-3	Sequence 3, Appl
44	104	54.7	488	4	US-09-367-777-44	Sequence 44, Appl
45	104	54.7	488	4	US-09-367-791A-27	Sequence 27, Appl

ALIGNMENTS

```
RESULT 1
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      87.9%; Score 167; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.3e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

Cy      1 ANAFLXXLRGSLXRCXKXQCSFXAXRXIFKDXRTKLFWISY 44
Db      1 ANAFLXXLRGSLXRCXKXQCSFXAXRXIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```

```
/ NAME/KEY: MOD RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```
Query Match      87.4%; Score 166; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.9e-21;
Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
```

RESULT 3

```
US-08-955-636-27
/ Sequence 27, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelsestuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 27
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```
Query Match      86.8%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 2.8e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
```

RESULT 4

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US-08-955-636-3
/ Sequence 3, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelsestuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
```

```
Query Match      86.3%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 4.2e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
```

```
RESULT 5
US-08-293-778-24
/ Sequence 24, Application US/08293778
/ Patent No. 5580560
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Nicolaesen, Else M.
/ APPLICANT: Bjorn, Soren E.
/ APPLICANT: Wlberg, Finn C.
/ APPLICANT: Woodbury, Richard
/ TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 55805600 No. 5580560disk of No. 55805600th America, Inc.
/ STREET: 405 Lexington Avenue, 62nd Floor
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10174-6201
```

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/293,778
/ FILING DATE:
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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/104,509
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/ FILING DATE: 25-JUN-1987
/ APPLICATION NUMBER: DK 3235/87
```

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/ FILING DATE: 25-JUN-1987
/ APPLICATION NUMBER: US 07/434,149
```

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/ FILING DATE: 13-NOV-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/DK88/00103
```

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/ FILING DATE: 24-JUN-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/898,248
```

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/ FILING DATE: 12-JUN-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Agis, Cheryl H.
```

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/ REGISTRATION NUMBER: 34,086
/ REFERENCE/DOCKET NUMBER: 3129, 224-US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-867-0123
```

```
/ TELEFAX: 212-867-0298
/ INFORMATION FOR SEQ ID NO: 24:
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TYPE: amino acid
```

```
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-293-778-24
```

```
Query Match      86.3%; Score 164; DB 1; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy      1 ANAFLXXLRQSLXRXCKXXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLYYLRPGSLYRCCKYQCSTFYVARYIFKDAVRTLFWISY 44
```

RESULT 6

```
US-08-295-411-5
```

```
; Sequence 5, Application US/08295411
; Patent No. 5679639
; GENERAL INFORMATION:
; APPLICANT: Griffith, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,411
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/793,989
; FILING DATE: 18-NOV-1991
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-295-411-5

Query Match      86.3%; Score 164; DB 1; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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QY      1 ANAFLLXLRQSLRXCKXQCSFXAXRIFKDXARTKLFWISY 44
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Db      1 ANAFLELRPGSLRBECKEQCSFEARERIFKDXARTKLFWISY 44
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RESULT 7
US-08-955-471-5
; Sequence 5, Application US/08955471
; Patent No. 5968751
; GENERAL INFORMATION:
; APPLICANT: Griffith, John H.
; APPLICANT: Meesters, Rolf M.
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
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; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/955,471
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/295,411
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR1263.0C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..152
; OTHER INFORMATION: /note= "Factor VII Light Chain"
; FEATURE:
; NAME/KEY: Region
; LOCATION: 153..406
; OTHER INFORMATION: /note= "Factor VII Heavy Chain"
; US-08-955-471-5

Query Match      86.3%; Score 164; DB 2; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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RESULT 8
PCT-US92-10242-5
; Sequence 5, Application PC/TUS9210242
; GENERAL INFORMATION:
; APPLICANT: Griffith, John H.
; APPLICANT: Meesters, Rolf
; TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
; TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
; TITLE OF INVENTION: for Inhibiting Coagulation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Office of Patent Counsel, The Scripps
; ADDRESSEE: Research Institute
; STREET: 10666 North Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
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/ COUNTRY: USA
/ ZIP: 92037
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/10242
/ FILING DATE: 19921118
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/793,989
/ FILING DATE: 18-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fitting, Thomas
/ REGISTRATION NUMBER: 34,163
/ REFERENCE/DOCKET NUMBER: SCR0472P
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-554-2937
/ TELEFAX: 619-554-6312
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 406 amino acids
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 1..152
/ OTHER INFORMATION: /note="Factor VII Light Chain"
/ FEATURE:
/ NAME/KEY: Region
/ LOCATION: 153..406
/ OTHER INFORMATION: /note="Factor VII Heavy Chain"
/ PCT-US92-10242-5
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Query Match 86.3%; Score 164; DB 5; Length 406;

Best Local Similarity 75.0%; Pred. No. 4.3e-20;

Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 1 ANAFLLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 44
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RESULT 9
US-08-475-845-2
/ Sequence 2, Application US/08475845
/ Patent No. 5788965
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Steuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: IBM PC compatible
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.24
/ CURRENT APPLICATION DATA:
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/ APPLICATION NUMBER: US/08/475,845
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
/ FILING DATE: 28-FEB-1991
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 13952-8-4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-475-845-2
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Query Match 86.3%; Score 164; DB 1; Length 444;

Best Local Similarity 75.0%; Pred. No. 4.7e-20;

Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy 1 ANAFLXLRQSLRXCKXQCSFYXAXIFKDAARTKLFWISY 44
Db 39 ANAFLLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 82
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RESULT 10
US-08-327-690-2
/ Sequence 2, Application US/08327690
/ Patent No. 5817788
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Steuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: IBM PC compatible
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/327,690
/ FILING DATE: 24-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
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FILED DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match 86.3%; Score 164; DB 2; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
DB 39 ANAFLELRPGSLRECKECCSFEEARLIFKDAERTKLFWISY 82

RESULT 11
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match 86.3%; Score 164; DB 2; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
DB 39 ANAFLELRPGSLRECKECCSFEEARLIFKDAERTKLFWISY 82

RESULT 12
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 86.3%; Score 164; DB 2; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44
DB 39 ANAFLELRPGSLRECKECCSFEEARLIFKDAERTKLFWISY 82

RESULT 13
US-08-671-003-2
Sequence 2, Application US/08871003
Patent No. 5997864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.

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/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Rasmussen, Mirella E.
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: ZymoGenetics, Inc.
/ STREET: 1201 Eastlake Avenue East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.24
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/ APPLICATION NUMBER: US/08/871,003
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sawislak, Deborah A.
/ REGISTRATION NUMBER: 37,438
/ REFERENCE/DOCKET NUMBER: 90-07C7
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-871-003-2

Query Match      86.3%; Score 164; DB 2; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSLLKXCKXQCSFXXRXIFKDAKRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEBCQSFEBAREIFKDAERTKLFWISY 82

RESULT 14
US-08-464-233-2
/ Sequence 2, Application US/08464233
/ Patent No. 6039944
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/464,233
/ FILING DATE:
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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/327,690
/ FILING DATE: 24-OCT-1994
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/662,920
/ FILING DATE: 28-FEB-1991
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parmelee, Steven W.
/ REGISTRATION NUMBER: 31,990
/ REFERENCE/DOCKET NUMBER: 13952-8-3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-467-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 444 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-464-233-2

Query Match      86.3%; Score 164; DB 3; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSLLKXCKXQCSFXXRXIFKDAKRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEBCQSFEBAREIFKDAERTKLFWISY 82

RESULT 15
US-09-189-607-2
/ Sequence 2, Application US/09189607
/ Patent No. 6168789
/ GENERAL INFORMATION:
/ APPLICANT: Berkner, Kathleen L.
/ APPLICANT: Petersen, Lars C.
/ APPLICANT: Hart, Charles E.
/ APPLICANT: Hedner, Ulla
/ APPLICANT: Bregengaard, Claus
/ TITLE OF INVENTION: Modified Factor VII
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Townsend and Townsend Kourie and Crew
/ STREET: One Market Plaza, Stuart Street Tower
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 94105-1492
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentln Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/189,607
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/660,289
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/327,690
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/065,725
/ FILING DATE: 21-MAY-1993
/ CLASSIFICATION:
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; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/662,920
 ; FILING DATE: 28-FEB-1991
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 13952-8-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-467-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 444 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-189-607-2

Query Match 86.3%; Score 164; DB 3; Length 444;
 Best Local Similarity 75.0%; Pred. No. 4.7e-20;
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXXLRQSLRXCKXXQCSFXAXRIFKDAARTLFWISY 44
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 Db 39 ANAFLEELRPGSLRECKCEQCSFEARBEIFKDAERTLFWISY 82

Search completed: July 28, 2003, 12:28:21
 Job time : 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:05 ; Search time 25 Seconds
(without alignments)
169.257 Million cell updates/sec

Title: SEQ4
Perfect score: 192
Sequence: 1 ANGFLXXLRGSLKRXCRXX.....XXAHXIFRNXXRTQPMVSY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	131	68.2	443	2 I46932	coagulation factor
3	123	64.1	466	1 KFH07	coagulation factor
4	107	55.7	461	1 JX0210	protein C (activat
5	106	55.2	461	1 S18994	protein C (activat
6	97	50.5	456	1 KXBO	protein C (activat
7	96	50.0	482	1 EXRT	coagulation factor
8	96	50.0	488	1 EXHU	coagulation factor
9	95	49.5	492	1 EXBO	coagulation factor
10	93	48.4	461	1 KFHU	coagulation factor
11	91	47.4	461	1 KXHU	protein C (activat
12	89	46.4	416	1 KRB0	coagulation factor
13	87	45.3	475	1 EXCH	coagulation factor
14	84	43.8	452	1 A00351	coagulation factor
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18	77	40.1	617	2 S10511	thrombin (EC 3.4.2
19	77	40.1	618	2 A35827	thrombin (EC 3.4.2
20	75	39.1	642	2 S53434	plasma protein S p
21	75	39.1	676	1 KXHUS	plasma protein S p
22	72	37.5	675	1 KXBOS	plasma protein S p
23	71	37.0	625	1 TBBO	thrombin (EC 3.4.2
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26	69	35.9	675	1 KXRTS	plasma protein S p
27	65	33.9	396	1 KXBOZ	plasma protein Z -
28	64	33.3	678	2 B48089	growth arrest-spec
29	63	32.8	673	2 A48089	growth arrest-spec

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31	61	31.8	674	2 I55476	growth potentiatin
32	52	27.1	605	1 M1WER	E1 protein - bovin
33	52	27.1	620	1 M1WRB2	E1 protein - bovin
34	51	26.6	413	1 VHWNIH	nucleoprotein - in
35	49.5	25.8	594	2 D84859	probable MAP kinase
36	49.5	25.8	603	2 G96753	probable MAP kinase
37	48.5	25.3	576	2 G96763	probable MAP kinase
38	45	23.4	687	2 T08528	O-antigen biosynth
39	45	23.4	1275	2 T18556	hypothetical prote
40	43	22.4	133	2 G81710	hypothetical prote
41	43	22.4	484	2 S43737	protein kinase SLT
42	43	22.4	1217	2 T21403	hypothetical prote
43	42	21.9	145	2 T42280	hypothetical prote
44	42	21.9	219	2 AE2449	hypothetical prote
45	42	21.9	242	2 AF1844	hypothetical prote

ALIGNMENTS

RESULT 1

KRB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <TAK>

R:McMullen, B.A.; Takikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:63308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCM>

A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Haee, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Contents: annotation

A:Note: structure and location of covalently bound carbohydrate

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAL>

F:1-44/Domain: Gla domain homology (fragment) <GLA>

F:50-81/Domain: EGF homology <EGF>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:52-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:63/Binding site: carbohydrate (Ser) (covalent) #status experimental

F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-Ile (coagulation factor X) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 81.8%; Score 157; DB 1; Length 407;
Best Local Similarity 70.5%; Pred. No. 9e-20;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

C>Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #ext_change 08-Dec-2000
 C/Accession: S49075; J04670; PS0191; PS0190; I62745
 R/Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
 Thromb. Res. 80, 63-73, 1995
 A>Title: Evidence for competition between vitamin K-dependent clotting factors for intra
 A/Reference number: A58496; PMID:96093366; PMID:8578533
 A/Accession: S49075
 A/Molecule type: mRNA
 A/Residues: 1-482 <ST1>
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A/Note: submitted to the EMBL Data Library, June 1994
 A/Note: neither the complete nucleic acid sequence nor the complete translation are show
 R/Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
 Gene 169, 269-273, 1996
 A>Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
 A/Reference number: J04670; PMID:96194815; PMID:8647460
 A/Accession: J04670
 A/Molecule type: mRNA
 A/Residues: 1-482 <ST1>
 A/Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
 A/Experimental source: Cos-1 cell
 R/Enyoji, K.; Miyazaki, K.; Kato, H.
 J. Biochem. 109, 890-898, 1991
 A>Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla
 A/Reference number: PS0190; PMID:92041742; PMID:1718949
 A/Accession: PS0191
 A/Molecule type: Protein
 A/Residues: 41-58, 'X', 60-65 <ENJ1>
 A/Accession: PS0190
 A/Molecule type: Protein
 A/Residues: 183-186, 'X', 188-207 <ENJ2>
 R/Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Nihno, Y.
 Eur. J. Haematol. 52, 162-168, 1994
 A>Title: Analysis of the partial nucleotide sequences and deduced primary structures of
 A/Reference number: 16196; PMID:94222160; PMID:9168596
 A/Accession: 162745
 A/Structure: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 295-383, 'G', 385-455 <MUR>
 A/Cross-references: GB:D1215; NID:9415309; PIDN:BA04756.1; PID:9455396
 C/Function:
 A>Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut
 F.1-23/Domain: signal sequence #status predicted <SIG>
 F.24-40/Domain: propeptide #status predicted <PRO>
 F.25-84/Domain: Gla domain homology <Gla>
 F.41-179/Product: coagulation factor X light chain #status predicted <LCH>
 F.90-121/Domain: EGF homology <EG1>
 F.129-164/Domain: EGF homology <EG2>
 F.183-482/Product: coagulation factor X heavy chain #status predicted <CH>
 F.189-231/Domain: activation peptide #status predicted <AP>
 F.233-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
 F.232-460/Domain: trypsin homology <TRY>
 F.46/47, 54, 56, 65, 66, 69, 72, 79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F.57-62, 90-101, 95-110, 112-121, 139-140, 136-149, 151-164, 172-174, 238-243, 259-275, 388-402, 41
 F.103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F.187/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F.208/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F.218/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.231-232/Cleavage site: Arg-18 (coagulation factor IXa, coagulation factor VIIa) #stat
 F.274, 330, 417/Active site: Arg-18, Asp, Ser #status predicted

Query Match 50.0%; Score 96; DB 1; Length 482;
 Best Local Similarity 36.4%; Pred. No. 6.3e-09;
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSILKXCRXXLCSFXXAHXIFRNXXRTQFWWSY 44
 Db 41 ANSPFEIKKGNLRECYBEICSPFEAREVDFENDEKTEFFMKY 84

RESULT 8

EXHU

coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N/Alternate names: Stuart factor

C/Species: Homo sapiens (man)

C/Date: 15-Nov-1984 #sequence revision 02-May-1994 #ext_change 08-Dec-2000

C/Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00

R/Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.

Biochemistry 25, 5098-5102, 1986

A>Title: Gene for human Factor X: a blood coagulation factor whose gene organization is e

A/Reference number: A24478; PMID:87026600; PMID:3768336

A/Accession: A24478

A/Molecule type: DNA

A/Residues: 1-488 <LEY>

A/Cross-references: GB:I29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:9182831

R/Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.

Gene 99, 291-294, 1991

A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag

A/Reference number: J00917; PMID:91216473; PMID:1902434

A/Accession: J00917

A/Molecule type: mRNA

A/Residues: 1-488 <MES>

A/Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:9182390

R/Miso, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.

J. Biol. Chem. 267, 7395-7401, 1992

A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagula

A/Reference number: A42485; PMID:92218390; PMID:1313796

A/Accession: A42485

A/Molecule type: DNA

A/Residues: 1-15 <MLA>

A/Experimental source: liver

A/Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)

R/Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.

Gene 41, 311-314, 1986

A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.

A/Reference number: A25853; PMID:86221713; PMID:3011603

A/Accession: A25853

A/Molecule type: mRNA

A/Residues: 19-284, 'E', 289-488 <KAU>

A/Cross-references: GB:M2613; NID:9180335; PIDN:AAA51984.1; PID:9180336

R/Pung, M.R.; Hay, C.W.; MacGillivray, R.T.A.

Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985

A>Title: Characterization of an almost full-length cDNA coding for human blood coagulat

A/Reference number: A22208; PMID:85216545; PMID:2582420

A/Accession: A22208

A/Molecule type: mRNA

A/Residues: 13-441, 'S', 443-488 <FUN>

A/Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:9182841

R/Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurachi, K.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984

A>Title: Characterization of a cDNA coding for human factor X.

A/Reference number: A21284; PMID:84222026; PMID:6587384

A/Accession: A21284

A/Molecule type: mRNA

A/Residues: 13-284, 'E', 289-488 <LE2>

A/Cross-references: GB:K01886

R/McMullen, T.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Wein

Biochemistry 22, 2875-2884, 1983

A>Title: Complete amino acid sequence of the light chain of human blood coagulation fac

A/Reference number: A20362; PMID:83257207; PMID:6871167

A/Accession: A20362

A/Molecule type: Protein

A/Residues: 41-179 <MCM>

R/Inoue, K.; Morita, T.

Eur. J. Biochem. 218, 153-163, 1993

A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of

A/Reference number: S39414; PMID:94062825; PMID:8243461

A/Accession: S39415

A/Molecule type: Protein

A/Residues: 183-234 <INO>

A/Note: glycosylation sites

A/Note: identification and characterization of beta-hydroxyaspartic acid

R/Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanham, K.; Lyman, G.

Gene 84f 517-519, 1989
 A/Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
 A/Reference number: 154051; MUID:90128299; PMID:2612918
 A/Accession: 154051
 A/Status: translation not shown; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-23 <RES>
 A/Cross-references: GB:M33297; NID:9183860; PID:AAA52636.1; PID:G553330
 R;Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bile
 J. Mol. Biol. 232, 947-966, 1993
 A/Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
 A/Reference number: A49458; MUID:93360277; PMID:8355279
 A/Contents: annotation; X-ray crystallography, 2.2 angstroms
 C/Comment: The two chains held together by one disulfide bond are formed from a single-c
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
 C/Genetics:
 A/Gene: GDB:F10
 A/Cross-references: GDB:119990; OMIM:227600
 A/Map position: 13q34-13q34
 A/Intons: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
 A/Note: deficiency of this factor causes Stuart disease
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 A/Pathway: blood coagulation
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-119/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-488/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-234/Domain: activation peptide #status experimental <APT>
 F:235-488/Product: coagulation factor Xa heavy chain #status experimental <ACT>
 F:235-462/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat
 F:57-62/Disulfide bonds: #status predicted
 F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:119,211/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental
 F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat
 F:216,222,419/Active site: His, Asp, Ser #status experimental

Query March 50.0%; Score 96; DB 1; Length 488;
 Best Local Similarity 36.4%; Pred. No. 6.4e-09;
 Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

1 ANGFLXXLRQGSILKRCXXLCSFXXAHXIPRNXXRTROPVNVSY 44
 41 ANSFLBEMKCHLRECEMETCTSYEARREVEDSDKTFEWNKY 84

EXBO
 coagulation factor Xa (BC 3.4.21.6) precursor - bovine
 N/Alternate names: Stuart factor
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999
 C/Accession: A22867; A14997; A12030; A34412; S39414; A00925
 R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
 Nucleic Acids Res. 12, 4481-4492, 1984
 A/Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a
 A/Reference number: A22867; MUID:84247315; PMID:6330671
 A/Accession: A22867
 A/Molecule type: mRNA
 A/Residues: 1-487 <FBN>
 A/Cross-references: GB:X00673; NID:q192; PIDN:CAA25286.1; PID:q193
 R;Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
 Biochemistry 19, 659-667, 1980
 A/Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
 A/Reference number: A14997; MUID:80130563; PMID:6766735

A/Accession: A14997
 A/Molecule type: protein
 A/Residues: 41-102 'N', 104-180 <BNF>
 R;McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A/Reference number: A20274; MUID:83308813; PMID:6688526
 A/Contents: annotation; revision to residue 103
 R;Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
 A/Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
 A/Reference number: A12030; MUID:76053069; PMID:1059093
 A/Accession: A12030
 A/Molecule type: protein
 A/Residues: 183-292,294-295 'GDE',299-334,336-348 'AE',351-354,356-441 'GKEG',446-492 <T
 A/Note: carboxylate binding sites and disulfide bonds were determined
 R;Persson, E.; Selander, M.; Limes, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
 J. Biol. Chem. 264, 16897-16904, 1989
 A/Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
 A/Reference number: A34412; MUID:89380326; PMID:2789221
 A/Accession: A34412
 A/Molecule type: protein
 A/Residues: 85-126 <PER>
 A/Note: beta-hydroxyaspartic acid site
 R;Inoue, K.; Morita, T.
 Eur. J. Biochem. 218, 153-163, 1993
 A/Title: Identification of O-linked oligosaccharide chains in the activation peptides of.
 A/Reference number: S39414; MUID:94062825; PMID:8243461
 A/Accession: S39414
 A/Molecule type: Protein
 A/Residues: 183-196,199-209,216-233 <INO>
 A/Note: carbohydrate binding sites
 R;Titani, K.; Hemmerson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; De
 Biochemistry 11, 4899-4903, 1972
 A/Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali
 A/Reference number: A12453; MUID:73053314; PMID:4264286
 A/Contents: annotation; active site
 R;Fujikawa, K.; Titani, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
 A/Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to f
 A/Reference number: A13504; MUID:76053121; PMID:1059122
 A/Contents: annotation; activation
 R;Sjog, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
 J. Biol. Chem. 259, 5705-5710, 1984
 A/Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic
 A/Reference number: A38024; MUID:84185716; PMID:6546930
 A/Contents: annotation; calcium binding
 R;Morita, T.; Jackson, C.M.
 J. Biol. Chem. 261, 4008-4014, 1986
 A/Reference number: A38025; MUID:86140210; PMID:3949800
 A/Contents: annotation; sulfate binding
 C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
 C/Comment: The two chains are formed from a single-chain precursor by the excision of tw
 C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), or
 activation.
 C/Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stron
 C/Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin
 C/Genetics:
 A/Gene: F10
 A/Map position: 13q34
 C/Function:
 A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-40/Domain: propeptide #status predicted <PRO>
 F:25-84/Domain: Gla domain homology <GLA>
 F:41-180/Product: coagulation factor X light chain #status experimental <LCH>
 F:90-121/Domain: EGF homology <EG1>
 F:129-164/Domain: EGF homology <EG2>
 F:183-492/Product: coagulation factor X heavy chain #status experimental <HCH>
 F:183-233/Domain: activation peptide #status experimental <APT>

F/234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>
 F/234-461/Domains: trypsin homology <TRY>
 F/46/47/54/56/59/60/65/66/69/72/75/79/Modified site: gamma-carboxyglutamic acid (Glu) #
 F/57-62/90-101/110-112/121/129-149/151-164/172-241/Disulfide bonds: #status F
 F/103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F/200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental
 F/208/488/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F/233-234/Cleavage site: Arg-11e (coagulation factor IX), coagulation factor VIIa) #stat
 F/240-245/260-276/389-403/414-442/Disulfide bonds: #status experimental
 F/275/321/418/Active site: His, Asp, Ser #status predicted

Query Match 49.5%; Score 95; DB 1; Length 492;
 Best Local Similarity 38.6%; Pred. No. 9.7e-09;
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 ANGFLLXLRQGLXKXCRXXLCSPFXKXHXIFNXXRTQFWSY 44
 Db 41 ANSFLEVKQGLNRECELEACSLSEAREVFEDADQTEFMSKY 84

RESULT 10
 KFHU
 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human
 N/Alternate names: antihemophilic factor B; Christmas factor
 C/Species: Homo sapiens (man)
 C/Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 15-Sep-2000
 A/Cross-references: A00922; A37570; A30511; A32989; A26273; A21337; A37546; A30623; A60486; A20
 R/Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 24, 3736-3750, 1985
 A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).
 A/Reference number: A00922; MUID:8600558; PMID:2994716
 A/Accession: A00922
 A/Molecule type: DNA
 A/Residues: 1-461 <XOS>
 A/Cross-references: GB:K02402; NID:g182612; PIDN:AA59620.1; PID:g182613
 R/Amson, D.S.; Choo, K.H.; Rees, D.J.G.; Giamelli, F.; Gould, K.; Huddleston, J.A.; Bro
 EMBO J. 3, 1053-1060, 1984
 A>Title: The gene structure of human anti-haemophilic factor IX.
 A/Reference number: A37570; MUID:84236100; PMID:6329734
 A/Accession: A37570
 A/Molecule type: DNA
 A/Residues: 1-461 <ANS>
 A/Cross-references: GB:K02048
 R/Reitsma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.
 Blood 72, 1074-1076, 1988
 A>Title: The putative factor IX gene promoter in hemophilia B Leyden.
 A/Reference number: A30511; MUID:88327116; PMID:3416069
 A/Accession: A30511
 A/Molecule type: DNA
 A/Residues: 8-24 <REI>
 A/Cross-references: EMBL:X55008; NID:g311288; PIDN:CA838245.2; PID:g4469253
 R/Koberl, D.D.; Boettma, C.D.K.; Buerstedde, J.M.; Sommer, S.S.
 Am. J. Hum. Genet. 45, 448-457, 1989
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor
 A/Reference number: A32989; MUID:89371752; PMID:2773937
 A/Accession: A32989
 A/Status: not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 30-92 <KOE>
 R/McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985
 A>Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat
 A/Reference number: A22673; MUID:85190593; PMID:3857619
 A/Accession: A22673
 A/Molecule type: mRNA
 A/Residues: 1-193, 'T', 195-461 <MCG>
 A/Cross-references: GB:M11309; NID:g180552; PIDN:AA52023.1; PID:g180553
 A/Note: the authors translated the codon ACA for residue 29 as Tyr
 R/Jaye, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Findeli, A.; Tolstosh
 Nucleic Acids Res. 11, 2325-2335, 1983
 A>Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba
 A/Reference number: A21337; MUID:8322078; PMID:6687940

A/Accession: A21337
 A/Molecule type: mRNA
 A/Residues: 1-193, 'T', 195-461 <JAY>
 A/Cross-references: GB:J00137; NID:g182610; PIDN:AA52763.1; PID:g182611
 R/Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.
 Somat. Cell Mol. Genet. 10, 465-473, 1984
 A>Title: Isolation and characterization of human factor IX cDNA: identification of Tag I
 A/Reference number: A37546; MUID:84300526; PMID:6089357
 A/Accession: A37546
 A/Molecule type: mRNA
 A/Residues: 38-193, 'T', 195-326 <JAG>
 A/Cross-references: GB:M35672
 R/Kurachi, K.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982
 A>Title: Isolation and characterization of a cDNA coding for human factor IX.
 A/Reference number: A30623; MUID:83065193; PMID:6959130
 A/Accession: A30623
 A/Molecule type: mRNA
 A/Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A', .
 A/Cross-references: GB:J00136; NID:g182608; PIDN:AA58726.1; PID:g182609
 A/Experimental source: liver
 R/Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.
 Vox Sang. 38, 21-29, 1990
 A>Title: Development of an immunoaffinity process for factor IX purification.
 A/Reference number: A60486; MUID:90194857; PMID:2316207
 A/Accession: A60486
 A/Molecule type: Protein
 A/Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>
 R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe
 A/Reference number: A20274; MUID:83308813; PMID:6688526
 A/Accession: A20274
 A/Molecule type: Protein
 A/Residues: 105-109, 'X', 111-115 <MCM>
 R/Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle
 Eur. J. Biochem. 172, 565-572, 1988
 A>Title: Characterisation of two differently processed forms of human recombinant factor
 A/Reference number: 50257; MUID:88166735; PMID:3280312
 A/Accession: 50257
 A/Molecule type: Protein
 A/Residues: 29-63 <BAL>
 A/Note: processed forms expressed in recombinant system
 R/Jallat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dietertle, A.; Faure, T.; Meullen, i
 EMBO J. 9, 3295-3301, 1990
 A>Title: Characterization of recombinant human factor IX expressed in transgenic mice an
 A/Reference number: S12058; MUID:91006024; PMID:2209546
 A/Accession: S12058
 A/Molecule type: mRNA; protein
 A/Residues: 1-68 <JAL>
 A/Note: processed forms expressed in recombinant system
 R/Hanford, P.A.; Barton, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell
 EMBO J. 9, 475-480, 1990
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium
 A/Reference number: S12377; MUID:90151623; PMID:2406139
 A/Accession: S12377
 A/Molecule type: protein
 A/Residues: 92-130 <HAN>
 A/Note: NMR detection of calcium binding by domain expressed in recombinant system
 R/de la Salle, C.; Charmanlier, J.L.; Baas, M.U.; Schwartz, A.; Wiesel, M.L.; Grunbaum,
 Thromb. Haemost. 70, 370-371, 1993
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi
 A/Reference number: 159612; MUID:94054330; PMID:8226150
 A/Accession: 159612
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 444-461 <RES>
 A/Cross-references: GB:S66752; NID:g439773; PIDN:AA82858.1; PID:g439774
 R/Stoffel, E.S.; Koeberl, D.D.; Sarker, G.; Sommer, S.S.
 Science 239, 491-494, 1988
 A>Title: Genomic amplification with transcript sequencing.
 A/Reference number: 159529; MUID:88127096; PMID:3340835
 A/Accession: 159529

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 290-359 <R2>
 A:Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182633
 R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw
 Biochemistry 33, 5167-5171, 1994
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lit
 A:Reference number: A54255; MUID:94227047; PMID:8172892
 A:Accession: A54255
 A:Molecule type: Protein
 A:Residues: 'D', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D', <AGA>
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.
 J. Clin. Invest. 61, 1528-1538, 1978
 A:Title: Activation of human factor IX (Christmas factor).
 A:Reference number: A18483; MUID:78194509; PMID:659613
 A:Contents: annotation; activation; active site; carbohydrate binding
 R:McGraw, R.A.; Davis, L.W.; Noyes, C.W.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984
 A:Reference number: A37569
 A:Contents: annotation
 A:Note: 194-Thr was also found
 R:Moritz, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 259, 5698-5704, 1984
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding
 A:Reference number: A37543; MUID:84185715; PMID:6425296
 A:Contents: annotation; calcium binding
 R:Moritz, T.; Isaacs, B.S.; Esmon, C.T.; Johnson, A.E.
 J. Biol. Chem. 260, 2583, 1985
 A:Reference number: A37544
 A:Contents: annotation; calcium binding, correction
 R:Berclay, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.
 Cell 45, 343-348, 1986
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation
 A:Reference number: A37545; MUID:86189947; PMID:3009023
 A:Contents: annotation; signal sequence cleavage site
 R:Sehito, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,
 J. Biol. Chem. 264, 21257-21265, 1989
 A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan
 A:Reference number: A30622; MUID:90078229; PMID:2592373
 A:Contents: annotation; sequence of mutant B(M) Nagoya
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle
 submitted to the Brookhaven Protein Data Bank, November 1991
 A:Reference number: A51252; PDB:1IXA
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130
 A:Note: recombinant form expressed in yeast
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
 C:Genetics:
 A:Gene: GDB:F9
 A:Cross-references: GDB:119900; OMIM:306900
 A:Map position: Xq27.1-Xq27.2
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1
 C:Function:
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese
 A:Pathway: blood coagulation intrinsic pathway
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:29-46/Domain: propeptide #status experimental <PP>
 F:31-91/Domain: Gla domain homology <GLA>
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:97-128/Domain: EGF homology <EG1>
 F:134-170/Domain: EGF homology <EG2>
 F:221-226/Domain: activation peptide #status experimental <ACT>
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>
 F:227-464/Domain: trypsin homology <TRY>
 F:523-54, 61, 63, 66, 67, 72, 73, 76, 79, 82, 86/Modified site: gamma-carboxyglutamic acid (Glu) #
 F:64-69, 97-108, 105-117, 119-128, 134-151, 141-155, 157-170, 178-335, 252-268, 382-396, 407-435/D
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental
 F:203, 213/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:205, 215/Binding site: carbohydrate (Thr) (covalent) #status experimental
 F:226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental
 Query Match 48.4%; Score 93; DB 1; Length 461;
 Best Local Similarity 41.9%; Pred. No. 2,1e-08;
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;
 QY 2 NGFLXLRGSLKRXCRXXLCSEFXAXHIXRNXRRQFVSVY 44
 Db 49 SGKLEFVQNLRECMERKSESEAREVENTERTEFTFKQY 91
 RESULT 11
 KKHU
 protein C (activated) (EC 3.4.21.69) precursor - human
 N:Alternate names: autoproteolysin IIA; plasma protein C
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
 C:Accession: A22331; A25426; A21781; A23789; A00927
 R:Poster, D.C.; Yoshitake, S.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985
 A:Title: The nucleotide sequence of the gene for human protein C.
 A:Reference number: A22331; MUID:85270390; PMID:2991887
 A:Accession: A22331
 A:Molecule type: DNA
 A:Residues: 1-461 <FOS1>
 A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986
 A:Title: Evolution and organization of the human protein C gene.
 A:Reference number: A25426; MUID:86120978; PMID:3511471
 A:Molecule type: DNA
 A:Residues: 1-445, 'L', 446-461 <PLU>
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332
 R:Poster, D.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984
 A:Title: Characterization of a cDNA coding for human protein C.
 A:Reference number: A21781; MUID:84272714; PMID:6589623
 A:Accession: A21781
 A:Molecule type: mRNA
 A:Residues: 'O', 107-461 <FOS2>
 A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323
 R:Beckmann, R.U.; Schmidt, R.U.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.
 Nucleic Acids Res. 13, 5233-5247, 1985
 A:Title: The structure and evolution of a 461 amino acid human protein C precursor and it
 A:Reference number: A23789; MUID:85269639; PMID:2991859
 A:Accession: A23789
 A:Molecule type: mRNA
 A:Residues: 1-461 <BEC>
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120
 R:Millerich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 265, 11397-11404, 1990
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me
 A:Reference number: A44605; MUID:50293094; PMID:1644179
 A:Contents: annotation; carbohydrate binding sites; activation peptide
 A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not
 R:Harris, R.U.; Ling, V.T.; Spellman, M.W.
 J. Biol. Chem. 267, 5102-5107, 1992
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor
 A:Reference number: A44606; MUID:92184750; PMID:1544884
 A:Contents: annotation; beta-hydroxyaspartic acid
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in
 C:Comment: Protein C is strongly enhanced by complexing with protein S. Protein C also fe
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
 bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
 C:Genetics:
 A:Gene: GDB:PROC
 A:Cross-references: GDB:120317; OMIM:176860
 A:Map position: 2q13-2q21
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding
 F:1-32/Domain: signal sequence #status predicted <Sig>
 F:27-86/Domain: Gla domain homology <Gla>
 F:33-42/Domain: propeptide #status predicted <Pro>
 F:43-197/Product: protein C light chain #status predicted <LCH>
 F:192-131/Domain: EGF homology <EG1>
 F:140-175/Domain: EGF homology <EG2>
 F:200-461/Product: protein C heavy chain #status predicted <HCH>
 F:200-211/Domain: activation peptide #status experimental <APt>
 F:212-445/Domain: trypsin homology <TRY>
 F:48-49,56,58,61,62,67,68,71/Modified site: gamma-carboxyglutamic acid (Glu) #status exp
 F:59-64,92-105,101-120,122-131,140-151,147-160,162-175,183-319,238-254,373-387,398-426/D
 F:106-111/Disulfide bonds: #status predicted
 F:110/Binding site: carbohydrate (Thr) (covalent) #status absent
 F:113/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:139,299,355/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:211-212/Cleavage site: Arg-Leu (trypsin) #status experimental
 F:253,299,402/Active site: His, Asp, Ser #status predicted
 F:371/Binding site: carbohydrate (Asn) (covalent) (partial) #status atypical

Query Match 47.4% Score 91; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 4,7e-08;
 Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANGLXLRQGSILXRCXRLCSFYXAHXIFRNXXRTQFWY 41
 Db 43 ANSFLERHSLSRECEIEICDFEAKEIFQVNDTLAIFW 83

RESULT 12

KFBO
 coagulation factor IXa (EC 3.4.21.22) precursor - bovine

N:Alternate names: Christmas factor

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Nov-1980 #sequence revision 03-Aug-1994 #text_change 16-Jul-1999

C:Accession: A14757; B20274; I45891; A00923

R:Katayama, K.; Erickson, L.H.; Enfield, D.L.; Walsh, K.A.; Neurath, H.; Davie, E.W.; Tl.
 Proc. Natl. Acad. Sci. U.S.A. 76, 4990-4994, 1979

A:Title: Comparison of amino acid sequence of bovine coagulation factor IX (Christmas fa
 A:Reference number: A14757; MUID:80056619; PMID:291916

A:Accession: A14757

A:Molecule type: protein

A:Residues: 1-63, 'T', 65-69 <KAT>

R:McMullen, B.A.; Fujikawa, K.; Kistel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co
 A:Reference number: A20274; MUID:83308813; PMID:6688526

A:Accession: B20274

A:Molecule type: protein

A:Residues: 59-63, 'X', 65-69 <MCM>

R:Choo, K.H.; Gould, K.G.; Rees, D.J.G.; Brownlee, G.G.

Nature 299, 178-180, 1982

A:Title: Molecular cloning of the gene for human anti-hemophilic factor IX.

A:Reference number: I45891; MUID:82272386; PMID:6287289

A:Accession: I45891

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 52-139 <CHO>

A:Cross-references: GB:J00007; NID:9163053; PIDN:AAA0520.1; PID:9163054

R:Haee, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
 A:Reference number: A44556; MUID:89213999; PMID:3149637

A:Contents: annotation

A:Note: structure and location of a carbohydrate covalently bound to Ser

C:Comment: Factor IX is activated by factor Xla, which excises the activation peptide pr

C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K

C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese

A:Pathway: blood coagulation intrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamic
 F:1-146/Product: coagulation factor IXa light chain #status experimental <ALC>
 F:1-45/Domain: Gla domain homology (fragment) <Gla>
 F:51-82/Domain: EGF homology <EG1>
 F:88-124/Domain: EGF homology <EG2>

F:147-181/Domain: activation peptide #status experimental <APt>
 F:182-416/Product: coagulation factor IXa heavy chain #status experimental <AHC>

F:182-409/Domain: trypsin homology <TRY>
 F:7,8,15,17,20,21,26,27,30,33,36,40/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:18-23,51-62,56-71,73-82,88-99,95-109,111-124,132-290,207-223,337-351,362-390/Disulfide
 F:53/Binding site: carbohydrate (Ser) (covalent) #status experimental

F:64/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
 F:158,168,173,261/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:222,270,366/Active site: His, Asp, Ser #status predicted

Query Match 46.4% Score 89; DB 1; Length 416;
 Best Local Similarity 37.2%; Pred. No. 9.6e-08;
 Matches 16; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Qy 2 NGFLXLRQGSILXRCXRLCSFYXAHXIFRNXXRTQFWY 44
 Db 3 SGKLEFPRGNLRECKEKSCSFEEAREVFENTETKTFWQY 45

RESULT 13

EXCH
 coagulation factor Xa (EC 3.4.21.6) precursor - chicken

N:Alternate names: vitru-activating proteinase

C:Species: Gallus gallus (chicken)

C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999

C:Accession: S15838; S20380; S20381

R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogatawara, T.; Naq

FEBS Lett. 283, 281-285, 1991

A:Title: Primary structure of the vitru activating protease from chick embryo. Its ident

A:Reference number: S15838; MUID:91257322; PMID:2044767

A:Accession: S15838

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-475 <STU>

A:Cross-references: DDBJ:D00844; NID:9222869; PIDN:BA00724.1; PID:9222870

R:Gotoh, B.; Yamauchi, F.; Ogatawara, T.; Nagai, Y.

FEBS Lett. 296, 274-278, 1992

A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib

A:Reference number: S20380; MUID:92164779; PMID:1537403

A:Accession: S20380

A:Molecule type: protein

A:Residues: 41-55 <GOT>

A:Accession: S20381

A:Molecule type: protein

A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>

C:Function:

A:Pathway: blood coagulation

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami

F:1-20/Domain: signal sequence #status predicted <Sig>

F:21-40/Domain: propeptide #status predicted <Pro>

F:25-84/Domain: Gla domain homology <Gla>

F:41-185/Product: coagulation factor X light chain #status experimental <LCH>

F:190-121/Domain: EGF homology <EG1>

F:129-167/Domain: EGF homology <EG2>

F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>

F:186-240/Domain: activation peptide #status predicted <APt>

F:241-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>

F:241-468/Domain: trypsin homology <TRY>

F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #stat

F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,423

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F:196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:282,328,425/Active site: His, Asp, Ser #status predicted

Query Match 45.3% Score 87; DB 1; Length 475;
 Best Local Similarity 36.4%; Pred. No. 2.4e-07;

Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
 Qy 1 ANGFLXXLRQSLKRCXXLCSPFXAXHIFRNXXRTROFWVSX 44
 Db 41 ANSLFEEMKQGNIRRECEBERCSFEAREAFEDNKEITEFWKQY 84

RESULT 14

coagulation factor IXa (EC 3.4.21.22) precursor - dog
 C:Species: Canis lupus familiaris (dog)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A30351; 146201
 R:Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.
 Blood 74, 207-212, 1989
 A>Title: Molecular cloning of a cDNA encoding canine factor IX.
 A:Reference number: A30351; MUID:89323338; PMID:2752110
 A:Accession: A30351
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-452 <EVA>
 A:Cross-references: GB:M21757; NID:g972719; PIDN:AAA75006.1; PID:g163948
 R:Abelrod, J.H.; Read, M.S.; Brinkhaus, K.M.; Verma, I.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990
 A>Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic
 A:Reference number: 146201; MUID:90311364; PMID:2367529
 A:Accession: 146201
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-452 <AXE>
 A:Cross-references: GB:M33826; NID:g163949; PIDN:AAA30844.1; PID:g163950
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-21/Domain: signal sequence #status predicted <PRO>
 F:22-40/Domain: propeptide #status predicted <SIG>
 F:24-84/Domain: Gla domain homology <GLA>
 F:41-452/Product: coagulation factor IX #status predicted <MAT>
 F:90-121/Domain: EGF homology <EG1>
 F:127-163/Domain: EGF homology <EG2>
 F:218-445/Domain: trypsin homology <TRY>
 F:46,47,54,56,59,60,65,66,69,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #
 F:57-62,90-101,95-110,112-121,127-138,134,150-163,171-326,243-259,373-387,398-426/Dist
 F:258,306,402/Active site: His, Asp, Ser #status predicted

Query Match 43.8%; Score 84; DB 1; Length 452;
 Best Local Similarity 37.2%; Pred. No. 7.9e-07;
 Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRQSLKRCXXLCSPFXAXHIFRNXXRTROFWVSX 44
 Db 42 SGKLEFVRGNLRECEBERCSFEAREAFEDNKEITEFWKQY 84

RESULT 15

coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
 C:Accession: J00419; 149667
 R:Wu, S.M.; Stafford, D.W.; Ware, J.
 Gene 86, 275-278, 1990
 A>Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.
 A:Reference number: J00419; MUID:90215309; PMID:2323576
 A:Accession: J00419
 A:Molecule type: mRNA
 A:Residues: 1-459 <WDS>
 A:Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158
 A:Experimental source: liver
 R:Sarkar, G.; Koeberl, D.D.; Sommer, S.S.
 Genomics 6, 133-143, 1990
 A>Title: Direct sequencing of the activation peptide and the catalytic domain of the fac
 A:Reference number: 146580; MUID:90152675; PMID:2303254
 A:Accession: 149667

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 168-362, 'O', 364-387, 'I', 389-451 <RS>
 A:Cross-references: GB:M26236; NID:g193319; PIDN:AAA37630.1; PID:g193320
 C:Comment: This protein plays a critical role in blood coagulation.
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>
 F:17-34/Domain: propeptide #status predicted <PRO>
 F:19-79/Domain: Gla domain homology <GLA>
 F:85-459/Product: coagulation factor IX #status predicted <MAT>
 F:85-116/Domain: EGF homology <EG1>
 F:122-158/Domain: EGF homology <EG2>
 F:225-452/Domain: trypsin homology <TRY>
 F:41,42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxylglutamic acid (Glu) #
 F:52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-286,380-394,405-433/Dist
 F:265,313,409/Active site: His, Asp, Ser #status predicted

Query Match 43.8%; Score 84; DB 2; Length 459;
 Best Local Similarity 37.2%; Pred. No. 8e-07;
 Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NGFLXXLRQSLKRCXXLCSPFXAXHIFRNXXRTROFWVSX 44
 Db 37 SGKLEFVRGNLRECEBERCSFEAREAFEDNKEITEFWKQY 79

Search completed: July 28, 2003, 12:25:27.
 Job time : 26 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:12:00 ; Search time 13.5 Seconds

(without alignments)
153.272 Million cell updates/sec

Title: SEQ4
Perfect score: 192
Sequence: 1 ANGFLXXLRGSLXRCRX.....XXAXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	81.8	407	FA7_BOVIN	P22457 bos taurus
2	131	68.2	444	FA7_RABIT	P98139 coryctolagus
3	123	64.1	466	FA7_HUMAN	P08709 homo sapien
4	113	58.9	218	TWGI_HUMAN	O14668 homo sapien
5	107	55.7	461	PRTC_MOUSE	P33587 mus musculu
6	106	55.2	446	FA7_MOUSE	P70375 mus musculu
7	106	55.2	461	PRTC_RAT	P31394 rattus norv
8	105	54.7	231	TWGI_HUMAN	O99122 sus scrofa
9	102	53.1	459	PRTC_PIG	O99122 sus scrofa
10	97	50.5	456	PRTC_BOVIN	P00742 homo sapien
11	96	50.0	488	FA10_HUMAN	P00743 bos taurus
12	95	49.5	492	FA10_BOVIN	P00743 bos taurus
13	94	49.0	490	FA10_RABIT	O19045 coryctolagus
14	93	48.4	461	FA9_HUMAN	P00740 homo sapien
15	91	47.4	461	PRTC_HUMAN	P04070 homo sapien
16	89	46.4	416	FA9_BOVIN	P00741 bos taurus
17	87	45.3	475	FA10_CHICK	P23155 gallus gall
18	84	43.8	452	FA9_CANFA	P19540 canis faml
19	84	43.8	458	PRTC_RABIT	O28661 coryctolagus
20	84	43.8	459	FA9_MOUSE	P12294 mus musculu
21	80	41.7	622	THRB_HUMAN	P00734 homo sapien
22	77	40.1	617	THRB_RAT	P18292 rattus norv
23	77	40.1	618	THRB_MOUSE	P18221 mus musculu
24	75	39.1	649	PRTS_MACRU	O28520 macaca mula
25	75	39.1	676	PRTS_BOVIN	P07225 bos taurus
26	72	37.5	675	PRTS_BOVIN	P07224 bos taurus
27	71	37.0	202	TWGI_HUMAN	O14669 homo sapien
28	71	37.0	625	THRB_BOVIN	P00735 bos taurus
29	71	37.0	646	PRTS_RABIT	P98118 coryctolagus
30	70	36.5	226	TWGI_HUMAN	O99246 homo sapien
31	69	35.9	376	FA10_TROCA	P81428 tropicodichis
32	69	35.9	400	PRTZ_HUMAN	P22891 homo sapien
33	69	35.9	675	PRTS_RAT	P53813 rattus norv

34	65	33.9	396	1	PRTZ_BOVIN	P00744 bos taurus
35	62	32.3	675	1	PRTS_MOUSE	O08761 mus musculu
36	52	27.1	604	1	VE1_BPV2	P11298 bovine papl
37	52	27.1	605	1	VE1_BPV1	P03116 bovine papl
38	51	26.6	413	1	NCAP_INNV	P16691 infectious
39	47.5	24.7	184	1	ADML_MOUSE	P97297 mus musculu
40	45	23.4	1275	1	RFBC_MYXXA	O50864 myxococcus
41	44	22.9	2812	1	ZAN_HUMAN	O39493 homo sapien
42	43	22.4	484	1	SLT2_YEARST	O00772 saccharomyc
43	42	21.9	320	1	GSHB_BUCAI	P57612 buchnera ap
44	42	21.9	345	1	VG59_HSV11	O00138 ictatuid h
45	41	21.4	529	1	VGLP_MEAST	P26031 measles vir

ALIGNMENTS

RESULT 1
FA7_BOVIN ID FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA Iwanaga S.,
RT "Bovine factor VII. Its purification and complete amino acid
RT sequence.",
RL J. Biol. Chem. 263:14868-14877(1988).
RN [2]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=9213999; PubMed=1149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.,
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX.",
RL J. Biochem. 104:867-868(1988).
RN [3]
RP STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.",
RL Adv. Exp. Med. Biol. 281:121-131(1990).
CC -I- FUNCTION: CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.
CC -I- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -I- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND.
CC -I- TISSUE SPECIFICITY: Plasma.
CC -I- PPM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM.
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -I- SIMILARITY: Contains 2 EGF-like domains.
DR PIR; A31979; KFB07.
DR HSSP; P08709; 1BF9.


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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR006209; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152
FT CHAIN 153 407
FT DOMAIN 6 35
FT DOMAIN 46 82
FT DOMAIN 87 128
FT DOMAIN 153 407
FT SITE 152 153
FT ACT_SITE 193 193
FT ACT_SITE 242 242
FT ACT_SITE 344 344
FT BINDING 338 338
FT DISULFID 17 22
FT DISULFID 50 61
FT DISULFID 55 70
FT DISULFID 72 81
FT DISULFID 91 102
FT DISULFID 98 112
FT DISULFID 114 127
FT DISULFID 135 262
FT DISULFID 159 164
FT DISULFID 178 194
FT DISULFID 310 329
FT DISULFID 340 368
FT MOD_RES 6 6
FT MOD_RES 7 7
FT MOD_RES 14 14
FT MOD_RES 16 16
FT MOD_RES 19 19
FT MOD_RES 20 20
FT MOD_RES 25 25
FT MOD_RES 26 26
FT MOD_RES 29 29
FT MOD_RES 35 35
FT CARBOHYD 52 52
FT CARBOHYD 145 145
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Query Match 81.8%; Score 157; DB 1; Length 407;
Best Local Similarity 70.5%; Pred No. 5.2e-21;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Oy 1 ANGFLXLRGSLXRCXRXIICSFYXAHXIFRNXXRTROFVSY 44
Db 1 ANGFLIEILLPSGLERECREELCSFEAEHIFRNEERTROFVSY 44

RESULT 2
FA7_RABBIT STANDARD; PRT; 444 AA.
AC P98139; P79224;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=93190306; PubMed=8383365;
RX Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII.";
RL Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U77477; AA837326.1; -.
DR HSRP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR006209; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.

```


DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KM Hydroxylase; Serine protease; Blood coagulation; zymogen; Glycoprotein;
Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 21
FT PROPEP 22 39
FT CHAIN 40 191
FT CHAIN 192 444
FT DOMAIN 45 74
FT DOMAIN 85 121
FT DOMAIN 126 167
FT DOMAIN 192 444
FT SITE 191 192
FT ACT_SITE 232 232
FT ACT_SITE 281 281
FT ACT_SITE 383 383
FT BINDING 377 377
FT DISULFID 56 61
FT DISULFID 89 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 130 141
FT DISULFID 137 151
FT DISULFID 153 166
FT DISULFID 174 301
FT DISULFID 198 203
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FT DISULFID 349 368
FT DISULFID 379 407
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FT MOD_RES 55 55
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FT MOD_RES 65 65
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FT MOD_RES 102 102
FT CARBOHYD 211 211
FT CARBOHYD 242 242
FT CARBOHYD 306 306
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5277F8 CRC64;
Query Match 68.2%; Score 131; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 3.3e-16;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator) (Eptacog alfa).
CN F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=66205965; PubMed=3486420;
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,
RA Davis E.W.;
RT "Characterization of a cDNA coding for human factor VII.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87260948; PubMed=3037537;
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
RA Hagen F.S., Murray M.O.;
RT "Nucleotide sequence of the gene coding for human factor VII, a
RT vitamin K-dependent protein participating in blood coagulation.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 61-466 AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=89088153; PubMed=3264725;
RA Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,
RA Pedersen A.H., Hedner U.;
RT "Amino acid sequence and posttranslational modifications of human
RT factor VIIa from plasma and transfected baby hamster kidney cells.";
RT Biochemistry 27:7785-7793(1988).
RN [5]
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
RX MEDLINE=91250411; PubMed=1904059;
RA Bjoern S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,
RA Komiyama Y., Pedersen A.H., Kistiel W.;
RT "Human plasma and recombinant factor VII. Characterization of O-
RT glycosylations at serine residues 52 and 60 and effects of site-
RT directed mutagenesis of serine 52 to alanine.";
RT J. Biol. Chem. 266:11051-11057(1991).
RN [6]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=90062160; PubMed=2511201;
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RA Shimomishi Y., Iwanaga S.;
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first
RT epidermal growth factor-like domain of human factors VII and IX and
RT protein Z and bovine protein Z.";
RT J. Biol. Chem. 264:20320-20325(1989).
RN [7]
RP STRUCTURE OF CARBOHYDRATE ON SER-112.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,
RA "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z.";
RT Adv. Exp. Med. Biol. 281:121-131(1990).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
RX MEDLINE=96175641; PubMed=8598903;
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;
RT "The crystal structure of the complex of blood coagulation factor
RT VIIa with soluble tissue factor.";
RT Nature 380:41-46(1996).

[9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.
 RA MEDLINE=99126538; PubMed=9925787;
 RA Zhang E., St Charles R., Tulinsky A.;
 RT "Structure of extracellular tissue factor complexed with factor VIIa
 RT inhibited with a BPT mutant.";
 RL J. Mol. Biol. 285:2089-2104(1999).
 RN (10)
 RP STRUCTURE BY NMR OF 105-145.
 RA MEDLINE=98367502; PubMed=9692950;
 RA Murenby A., Finn B.E., Gipeert G.P., Forren S., Stenflo J.,
 RA Drakenberg T.;
 RT "Solution structure of the N-terminal EGF-like domain from human
 RT factor VII.";
 RL Biochemistry 37:10605-10615(1998).
 RN (11)
 RP VARIANT GLN-364.
 RA MEDLINE=91300046; PubMed=2070047;
 RA O'Brien D.P., Gale K.W., Anderson J.S., McVey J.H., Miller G.J.,
 RA Meade T.W., Tuddenham E.G.D.;
 RT "Purification and characterization of factor VII 304-Gln: a variant
 RT molecule with reduced activity isolated from a clinically unaffected
 RT male.";
 RL Blood 78:132-140(1991).
 RN (12)
 RP VARIANTS GLN-364 AND PHE-370.
 RA MEDLINE=92340074; PubMed=1634227;
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,
 RA Roderigo G., Casonato A., Girolami A., Bernardi F.;
 RT "Detection of two missense mutations and characterization of a repeat
 RT polymorphism in the factor VII gene (F7).";
 RL Hum. Genet. 89:497-502(1992).
 RN (13)
 RP VARIANT TYR-238.
 RA MEDLINE=93372811; PubMed=8364544;
 RA Marchetti G., Ferrati M., Patrascchini P., Redaelli R., Bernardi F.;
 RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms
 RT (115His and 333Ser) in the human coagulation factor VII gene.";
 RL Hum. Mol. Genet. 2:1055-1056(1993).
 RN (14)
 RP VARIANTS.
 RA MEDLINE=94061028; PubMed=8242057;
 RA Takamiya O., Kemmell-Cook G., Martin D.M.A., Cooper D.N.,
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
 RA Tuddenham E.G.D., McVey J.H.;
 RT "Detection of missense mutations by single-strand conformational
 RT polymorphism (SSCP) analysis in five dysfunctional variants of
 RT coagulation factor VII.";
 RL Hum. Mol. Genet. 2:1355-1359(1993).
 RN (15)
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.
 RA MEDLINE=94264305; PubMed=8204879;
 RA Chaling S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,
 RA Roberts H.R., Blajchman M., Monroe D.W., High K.A.;
 RT "Severe factor VII deficiency caused by mutations abolishing the
 RT cleavage site for activation and altering binding to tissue factor.";
 RL Blood 83:3524-3535(1994).
 RN (16)
 RP VARIANT VAL-354.
 RA MEDLINE=95072589; PubMed=7981691;
 RA Bernardi F., Caetanani G., Redaelli R., Pinotti M., Lunghi B.,
 RA Rodeghiero F., Marchetti G.;
 RT "Topologically equivalent mutations causing dysfunctional coagulation
 RT factors VII (294Ala->Val) and X (334Ser->Pro).";
 RL Hum. Mol. Genet. 3:1175-1177(1994).
 RN (17)
 RP VARIANT WIE HIS-307.
 RA MEDLINE=95064662; PubMed=7974346;
 RA Ohnwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
 RA Suzuki K.;
 RT "Factor VII: heterozygous asymptomatic type I deficiency caused by
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
 RT catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).
 RN (18)
 RP VARIANT MET-419.
 RA MEDLINE=96247510; PubMed=8652821;
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;
 RT "A Thr35Met mutation in factor VII of a patient with a hereditary
 RT deficiency causes defective secretion of the molecule.";
 RL Blood 87:5085-5094(1996).
 RN (19)
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.
 RA MEDLINE=97001216; PubMed=8844208;
 RA Bernardi F., Caetanani G., Pinotti M., Ferrarese P., di Iasio M.G.,
 RA Lunghi B., Rodeghiero F., Marchetti G.;
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII
 RT deficiency.";
 RL Hum. Mutat. 8:108-115(1996).
 RN (20)
 RP VARIANT VAL-304.
 RA MEDLINE=97037613; PubMed=8883260;
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostichevsky M.,
 RA Zaitov R., Seligson U.;
 RT "A18244Val is a common, probably ancient mutation causing factor VII
 RT deficiency in Moroccan and Iranian Jews.";
 RL Thromb. Haemost. 76:283-291(1996).
 RN (21)
 RP VARIANT MORIOKA PRO-13.
 RA MEDLINE=98235713; PubMed=9576180;
 RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,
 RA Sakuragawa N.;
 RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in
 RT the signal sequence identified in a patient with factor VII
 RT deficiency.";
 RL Br. J. Haematol. 101:47-49(1998).
 RN (22)
 RP VARIANTS MALTA THR-194 AND VAL-304.
 RA MEDLINE=98112461; PubMed=9452082;
 RA Alshinawi C., Secchi C., Galdies R., Aquilina A., Felice A.E.;
 RT "Two new missense mutations (P134T and A244V) in the coagulation
 RT factor VII gene.";
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).
 RN (23)
 RP VARIANTS ASP-295 AND GLN-413.
 RA MEDLINE=99318093; PubMed=10391209;
 RA Gargill M., Altshuler D., Ireland J., Sklar P., Ardile K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 Query Match 64.1%; Score 123; DB 1; Length 466;
 Best Local Similarity 52.3%; Pred. No. 1e-14;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
 Cyt 1 ANGFLXLLRGGSLXRCRXLLCSFXHXHFERXXRFRQWVY 44
 Db 61 ANAFLELRPSLERECKECSEFARERIFKDAERTKLPWISY 104
 RESULT 4
 TMGL_HUMAN STANDARD; PRT; 218 AA.
 AC O1468;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
 DE rich gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
 DE 1).
 GN PRG1 OR TMG1 OR PRGP1.
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kullman U.D., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; 1CFH.
DR Genew; HGNC:9469; PRG1.
DR MIM; 604428; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR00294; VltK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GUU_CARBOXYLATION; 1.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 84 106 POTENTIAL.
FT DOMAIN 107 218 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 61 GLA-RICH.
FT DOMAIN 131 135 POLY-PRO.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61ABA0A98 CRC64;

Query Match 58.9%; Score 113; DB 1; Length 218;
Best Local Similarity 40.9%; Pred. No. 3,1e-13;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANGFLXLLROGSLKRXCRXXLCSPFXAHXIPRNXXRTROFVNVSY 44
Db 21 ANGFEIRIQNIRKECKEETPEAREAPENNEKTEFWSTY 64

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RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein C cDNA."
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nino Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C."
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIa
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GUU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC -----
DR EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; D43755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_lke.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00008; trypsin; 1.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYF_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 319
FT DISULFID 238 254
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 214 214
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CONFLICT 328 328
FT CONFLICT 393 393
SQ SEQUENCE 461 AA; 51945 MW; 53PAA0D85B194D6E CRC64;

Query Match 55.7%; Score 107; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 8.6e-12;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

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QY 1 ANGFLXLRGSLKRXCRXLCSFXAXHIFRNXXRTQFWVSY 44
Db 42 ANSFLEMRPSLSRECHMEICDFEBAQEIFQNVEDTLAFWKY 85

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RESULT 6
ID_FAY MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Created)

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127167; PubMed=8972017;
RA Idusogie E., Rosen B.D., Carmeliet P., Collen D., Caetzelino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964 (1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PTM: THE VITAMIN K-DEPENDENT. ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC -----
DR EMBL; U66079; AAC3796.1; -.
DR HSSP; P08709; 1BP9.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001481; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00169; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_CA; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;

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KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT PROPEP 25 41 POTENTIAL.
 FT CHAIN 42 193 FACTOR VII LIGHT CHAIN.
 FT CHAIN 194 446 FACTOR VII HEAVY CHAIN.
 FT DOMAIN 47 76 GLA-RICH.
 FT DOMAIN 87 123 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 128 169 EGF-LIKE 2.
 FT DOMAIN 194 446 SERINE PROTEASE.
 FT SITE 193 194 CLEAVAGE (BY FACTOR XA, FACTOR XIa,
 ACT_SITE 234 234 FACTOR IXa, OR THROMBIN) (BY SIMILARITY).
 ACT_SITE 283 283 BY SIMILARITY.
 ACT_SITE 385 385 BY SIMILARITY.
 BINDING 379 379 BY SIMILARITY.
 DISULFID 58 63 SUBSTRATE (BY SIMILARITY).
 DISULFID 91 102 BY SIMILARITY.
 DISULFID 96 111 BY SIMILARITY.
 DISULFID 113 122 BY SIMILARITY.
 DISULFID 132 143 BY SIMILARITY.
 DISULFID 139 153 BY SIMILARITY.
 DISULFID 155 168 BY SIMILARITY.
 DISULFID 176 303 BY SIMILARITY.
 DISULFID 200 205 BY SIMILARITY.
 DISULFID 219 235 BY SIMILARITY.
 DISULFID 351 370 BY SIMILARITY.
 DISULFID 381 409 BY SIMILARITY.
 MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
 MOD_RES 104 104 HYDROXYLATION (BY SIMILARITY).
 CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 446 AA; 50276 MW; 2512E44A45C8C96E CRC64;

Query Match 55.2%; Score 106; DB 1; Length 446;
 Best Local Similarity 47.7%; Pred. No. 1.3e-11;
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSILKRCXXLCSFXAXHIFRNXXRTROFVWSY 44
 42 ANSLBELWPGSLRECNBECSEBARERFKSPERTIKQFIIVY 85

Db 1 ANGFLXXLRQGSILKRCXXLCSFXAXHIFRNXXRTROFVWSY 44
 42 ANSLBELWPGSLRECNBECSEBARERFKSPERTIKQFIIVY 85

RESULT 7
 PRTC_RAT STANDARD; PRT; 461 AA.
 ID AC P1354;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
 DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation factor XIV).
 GN PROC.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar; TISSUE=Liver;
 RX MEDLINE=92329550; PubMed=1627650;
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
 RT "The cDNA cloning and mRNA expression of rat protein C.";

RL Biochim. Biophys. Acta 1131:329-332(1992).
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
 CC REGULATE BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
 CC and VIIa.
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
 CC TETRAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS IS
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
 CC STRONGLY PROMOTED BY THROMBOMODULIN.
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
 CC THROMBIN-THROMBOMODULIN COMPLEX.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -----
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 CC -----
 CC EMBL; X64336; CAA45617.1; -;
 CC PIR; S18994; S18994.
 CC HSP; P04070; 1PCU.
 CC MEROPS; S01.218; -;
 CC Interpro; IPR000152; Asx_hydroxyl.
 CC Interpro; IPR001314; Chymotrypsin.
 CC Interpro; IPR001881; EGF Ca.
 CC Interpro; IPR006209; EGF_Like.
 CC Interpro; IPR002383; GLA_blood.
 CC Interpro; IPR001254; Ser_protease_Try.
 CC Interpro; IPR000294; VitK_dep_GLA.
 CC Pfam; PF00008; EGF; 2.
 CC Pfam; PF00594; Gla; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00001; GLABLOOD.
 CC SMART; SM00069; GLA; 1.
 CC SMART; SM00020; TRYD_SPC; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS01187; EGF CA; 1.
 CC PROSITE; PS00011; GLU CARBOXYLATION; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Blood coagulation; Glycoprotein; Serine protease;
 CC Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 CC EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 32
 FT PROPEP 33 41
 FT CHAIN 42 196
 FT CHAIN 199 461
 FT PEPTIDE 199 212
 FT SITE 212 213
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 213 461
 MOD_RES 47 47
 MOD_RES 48 48

BY SIMILARITY.
 BY SIMILARITY.
 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
 ACTIVATION PEPTIDE (BY SIMILARITY).
 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
 EGF-LIKE 1.
 EGF-LIKE 2.
 SERINE PROTEASE.
 GAMMA-CARBOXYGLUTAMIC ACID
 (BY SIMILARITY).
 GAMMA-CARBOXYGLUTAMIC ACID
 (BY SIMILARITY).

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FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 112 112 (BY SIMILARITY).
FT ACT_SITE 254 254 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;
```

```
Query Match 55.2%; Score 106; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.3e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
```

```
Oy 1 ANGFLXLRQSLKRCXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 42 ANSFLEELRQGTIERECMEETCSYEVEKVEFENKXETFEWKGY 85
```

```
RESULT 8
TMG3_HUMAN STANDARD; PRT; 231 AA.
AC Q9BZD7;
```

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Transmembrane gamma-carboxyglutamic acid protein 3 precursor.

TMG3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

RC TISSUE=Spinal cord;

RE MEDLINE=2117044; PubMed=11171957;

RA Kulman J.D., Harris J.E., Xie L., Davie E.W.;

RT "Identification of two novel transmembrane gamma-carboxyglutamic acid

RT proteins expressed broadly in fetal and adult tissues.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).

CC -1 SUBCELLULAR LOCATION: Type I membrane protein.

CC -1 TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.

CC -1 PTM: Gla residues are produced after subsequent posttranslational

CC modifications of glutamic acid by a vitamin K-dependent gamma-

CC carboxylase.

CC -----

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CC -----

CC EMBL; AF326350; AAK0955.1; -.

DR HSSP; P00740; ICFH.

DR GO; GO:0016021; C:Integral to membrane; NAS.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00594; gla; 1.

DR SMART; SM0069; GLA; 1.

DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.

KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.

FT PROPEP 1 19 POTENTIAL.

FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID

FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 79 101 POTENTIAL.

FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 23 60 GLA-RICH.

SQ SEQUENCE 231 AA; 25848 MW; 8A373E4848490D81 CRC64;

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Query Match 54.7%; Score 105; DB 1; Length 231;
Best Local Similarity 40.9%; Pred. No. 9.6e-12;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
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Oy 1 ANGFLXLRQSLKRCXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 20 ANSFLEELRQGTIERECMEETCSYEVEKVEFENKXETFEWKGY 63
```

RESULT 9

PTC_PIG STANDARD; PRT; 459 AA.

AC Q9GFP2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT Vitamin-K-dependent protein C precursor (EC 3.4.21.69)

DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation

DE factor XIV).

GN PROC.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI_TaxID=9623;

[1]

SEQUENCE FROM N.A.

RC TISSUE=Liver;

RE MEDLINE=21121490; PubMed=11229814;

RA Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,

RA Kim H.K.W.;

RT "Porcine Factor V: cDNA cloning, gene mapping, three-dimensional

RT protein modelling of membrane binding sites and comparative anatomy of

RT domains.";

RL Cell. Mol. Life Sci. 58:148-159(2001).

CC -1 FUNCTION: Protein C is a vitamin K-dependent serine protease that

CC regulates blood coagulation by inactivating factors Va and VIIIa

CC in the presence of calcium ions and phospholipids.

CC -1 CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va

CC and VIIIa.

CC -1 SUBUNIT: Synthesized as a single chain precursor, which is cleaved

CC into a light chain and a heavy chain held together by a disulfide

CC bond. The enzyme is then activated by thrombin, which cleaves a

CC tetradecapeptide from the amino end of the heavy chain; this

CC reaction, which occurs at the surface of endothelial cells, is

CC strongly promoted by thrombomodulin.

CC -1 TISSUE SPECIFICITY: Plasma; synthesized in the liver.

CC -1 PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu

CC residues allows the modified protein to bind calcium.

CC -1 MISCELLANEOUS: Calcium also binds, with stronger affinity to

CC another site, beyond the GLA domain. This GLA-independent binding

CC site is necessary for the recognition of the
 CC thrombin-thrombomodulin complex.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -----
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 CC -----
 DR HESBP; AF191307; AAG28380.1; -.
 DR HESBP; P04070; IPCU.
 DR MEROPS; S01.218; -.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; G1a; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; TRYR_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS05240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Blood coagulation; Glycoprotein; Serine protease;
 DR Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
 DR EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 41
 FT CHAIN 42 459
 FT CHAIN 42 196
 FT CHAIN 199 459
 FT CHAIN 199 213
 FT SITE 213 214
 FT DOMAIN 96 131
 FT DOMAIN 135 175
 FT DOMAIN 214 459
 FT MOD_RRS 47 47
 FT MOD_RRS 48 48
 FT MOD_RRS 55 55
 FT MOD_RRS 57 57
 FT MOD_RRS 60 60
 FT MOD_RRS 61 61
 FT MOD_RRS 66 66
 FT MOD_RRS 67 67
 FT MOD_RRS 70 70

FT MOD_RES 112 112
 FT ACT_SITE 255 255
 FT ACT_SITE 301 301
 FT ACT_SITE 400 400
 FT DISULFID 58 63
 FT DISULFID 91 110
 FT DISULFID 100 105
 FT DISULFID 104 119
 FT DISULFID 121 130
 FT DISULFID 139 150
 FT DISULFID 146 159
 FT DISULFID 161 174
 FT DISULFID 182 321
 FT DISULFID 240 256
 FT DISULFID 371 385
 FT DISULFID 396 424
 FT CARBOHYD 138 138
 FT CARBOHYD 292 292
 FT CARBOHYD 353 353
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
 Query Match 53.1%; Score 102; DB 1; Length 459;
 Best Local Similarity 45.5%; Pred. No. 7; Ie-11;
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;
 QY 1 ANGELIXXLRGSLXRCRXXLCSFXAHXIFRXXXTROQWVSX 44
 DB 42 ANSFLELRPSLSRECKERTCDPEARLEIFONTENTMAWMSKY 85
 RESULT 10
 PRTC_BOVIN STANDARD; PRT; 456 AA.
 AC P00745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vitamin-K-dependent protein C precursor (BC 3.4.21.69)
 DE (Autoproteolytic cleavage)
 DE (Anticoagulant protein C) (Blood coagulation
 factor XIV) (Fragment).
 GN PROC.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85014826; PubMed=6091100;
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.,
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
 RN [2]
 RP SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITES ASN-136.
 RX MEDLINE=83007325; PubMed=6896876;
 RA Fernlund P., Stenflo J.,
 RT "Amino acid sequence of the light chain of bovine protein C";
 RL J. Biol. Chem. 257:12170-12179(1982).
 RN [3]
 RP REVISION TO 110.
 RX MEDLINE=83169769; PubMed=6572939;
 RA Drakenberg T., Fernlund P., Koepsch P., Stenflo J.,
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
 RN [4]
 RP SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
 RX AND ASN-366.
 RX MEDLINE=83007326; PubMed=6896877;
 RA Stenflo J., Fernlund P.,
 RT "Amino acid sequence of the heavy chain of bovine protein C";
 RL J. Biol. Chem. 257:12180-12190(1982).
 RN [5]


```

RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmen N.L., Debaule L.E., Esmen C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RL J. Biol. Chem. 258:5548-5553 (1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmen N.L., Laue T.M., Esmen C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560 (1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
-----
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CC EMBL; K02435; AAA30685.1; -.
DR PIR; A26250; KXBO.
DR HSSP; P04070; LPCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

```

```

KW EGF-like domain; Repeat; Endothelial cell; Hydroxylase; Signal.
FT NON_TER 1
FT SIGNAL <1 29
FT PROPEP 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 62 62
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 110 110
FT ACT_SITE 252 252
FT ACT_SITE 298 298
FT ACT_SITE 397 397
FT DISULFID 56 61
FT DISULFID 89 108
FT DISULFID 98 103
FT DISULFID 102 117
FT DISULFID 119 128
FT DISULFID 137 148
FT DISULFID 144 157
FT DISULFID 159 172
FT DISULFID 180 318
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136
FT CARBOHYD 289 289
FT CARBOHYD 350 350
FT CARBOHYD 366 366
FT VARIANT 82 82
FT VARIANT 82 82
FT CONFLICT 455 456
FT SEQUENCE 456 AA; 51407 MM; CAA6833F894C209 CRC64;

Query Match 50.5%; Score 97; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 5.8e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRQSLKRXCRXXLCSPFXAHXIFRNXXRFRQFWVS 44
Db 40 ANSLFLELRGQNVRECESEVCEFEAREBIFQNTEDIMARFSF 83

RESULT 11
ID FA10 HUMAN STANDARD; PRT; 488 AA.
AC P00742; Q14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91216473; PubMed=1902434.
RX Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";

```


RN Gene 99:291-294(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87026600; PubMed=3768336;
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
 RT "Gene for human factor X: a blood coagulation factor whose gene
 RT organization is essentially identical with that of factor IX and
 RT protein C.";
 RL Biochemistry 25:5098-5102(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Ozuna M., Pool C.L., Toch E.J., Yi Q., Nickerson D.A.;
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 13-488 FROM N.A.
 RX MEDLINE=85216545; PubMed=2582420;
 RA Fung M.R., Hay C.W., McGilivray R.T.A.;
 RT "Characterization of an almost full-length cDNA coding for human
 RT blood coagulation factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
 RN [5]
 RP SEQUENCE OF 19-488 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86221713; PubMed=3011603;
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
 RT "Isolation and characterization of human blood-coagulation factor X
 RT cDNA.";
 RL Gene 41:311-314(1986).
 RN [6]
 RP SEQUENCE OF 41-179.
 RX MEDLINE=83257207; PubMed=6671167;
 RA McMillen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howard W.N.,
 RA Kwa E.Y., Weinstein B.;
 RT "Complete amino acid sequence of the light chain of human blood
 RT coagulation factor X: evidence for identification of residue 63 as
 RT beta-hydroxyaspartic acid.";
 RL Biochemistry 22:2875-2884(1983).
 RN [7]
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=84222026; PubMed=6587384;
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor X.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
 RN [8]
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=94062825; PubMed=8243461;
 RA Inoue K., Morita T.;
 RT "Identification of O-linked oligosaccharide chains in the activation
 RT peptides of blood coagulation factor X. The role of the carbohydrate
 RT moieties in the activation of factor X.";
 RL Eur. J. Biochem. 218:155-163(1993).
 RN [9]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE=90128299; PubMed=2612918;
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;
 RT "Cloning and characterization of the 5' end (exon 1) of the gene
 RT encoding human factor X.";
 RL Gene 84:517-519(1989).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=93360277; PubMed=8355279;
 RA Padmanabhan K., Padmanabhan K.P., Tulineky A., Park C.H., Bode W.,
 RA Huber R., Blankenship D.T., Gardin A.D., Kistiel W.;
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
 RL J. Mol. Biol. 232:947-966(1993).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
 RX MEDLINE=98283982; PubMed=96198463;
 RA Kanata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
 RT "Structural Basis for Chemical Inhibition of human blood coagulation
 RT factor Xa."

```

RU Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
RN [12]
RP VARIANTS ILE-7 AND HIS-30.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanarman N., Nemes J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes."
RL Nat. Gene. 22:231-238(1999).
RV [13]
RP ERRATUM.
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanarman N., Nemes J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC -----
DR EMBL; K03194; AAA52490.1; -.
DR EMBL; M57285; AAA52421.1; -.
DR EMBL; AF503510; ANM19347.1; -.
DR EMBL; U29433; AAA52764.1; -.
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DR EMBL; L00392; AAA52764.1; JOINED.
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DR EMBL; M22613; AAA51984.1; -.
DR EMBL; K01886; AAA52486.1; -.
DR EMBL; M33297; AAA52636.1; -.
DR PIR; A24478; EXHU.
DR PDB; 1HCG; 08-MAY-95.
DR PDB; 1FAX; 29-OCT-97.
DR PDB; 1FXV; 17-JUN-98.
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DR PDB; 1XKB; 23-MAR-99.
DR PDB; 1EQZ; 20-SEP-00.
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DR PDB; 1FOS; 20-SEP-00.
DR PDB; 1FJS; 17-NOV-00.
DR PDB; 1G2L; 20-OCT-01.
DR PDB; 1G2M; 20-OCT-01.
DR PDB; 1KSN; 19-JUN-02.
DR PDB; 1KYE; 11-FEB-03.
DR PDB; 1MO5; 28-JAN-03.

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DR PDB; 1MO6; 28-JAN-03.
DR PDB; 1NFU; 25-FEB-03.
DR PDB; 1NFV; 25-FEB-03.
DR PDB; 1NFY; 25-FEB-03.
DR PDB; 1NFY; 25-FEB-03.
DR MEROPS; S01.216; -.
DR GlycoSiteDB; P00742; -.
DR Genew; HGNC:3528; F10.
DR MIM; 134530; -.
DR MIM; 227600; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0003804; F:blood coagulation factor X activity; TAS.
DR GO; GO:0007356; P:blood coagulation; TAS.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001861; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

Query March 50.0%; Score 96; DB 1; Length 488;
Best Local Similarity 36.4%; Pred. No. 9.5e-10;
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QY 1 ANGFLXXLRQSLRXCRXLCSFYXAHXIFRNXXRTQFVWSY 44
Db 41 ANSFLBEMKXGHLBECMEBETCSYEAREVEEDSDKTNFNNKY 84

RESULT 12
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DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
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RP SEQUENCE OF 1-487 FROM N.A.
RX MEDLINE=84247315; PubMed=6330671;
RA Fung W.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;*
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RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6685526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson W.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Suo T., Bjork I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SUBUNITON.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and X2 to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).
```

RN [12]
 RP STRUCTURE BY NMR OF 85-126.
 RX MEDLINE=92406922; PubMed=1527084;
 RA Selander-Sunneberg M., Ullner M., Persson E., Teleman O.,
 RA Stenflo J., Drakenberg T.,
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-
 RT like domain in coagulation factor X.",
 RL J. Biol. Chem. 267:19642-19649(1992).
 RN [13]
 RP STRUCTURE BY NMR OF 41-126.
 RX MEDLINE=96387194; PubMed=8794734;
 RA Sunneberg M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
 RA Trewhella J.,
 RT "The relative orientation of Gla and EGF domains in coagulation
 RT factor X is altered by Ca2+ binding to the first EGF domain. A
 RT combined NMR-small angle X-ray scattering study.",
 RL Biochemistry 35:11547-11559(1996).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -----
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 CC EMBL: X00673; CAA25286.1; -.
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 DR PDB; IAPQ; 3I-JAN-94.
 DR PDB; IICF; 3I-MAY-94.
 DR PDB; IMHE; 15-MAY-97.
 DR PDB; IMHF; 15-MAY-97.
 DR PDB; IIOD; 2I-JAN-03.
 DR PDB; IKIG; 28-OCT-98.
 DR MEROPS; S01.216; -.
 DR GlycoSuiteDB; P00743; -.
 DR InterPro; IPR000152; Asx_hydroxyl-
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; GLA_Like.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
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 DR SMART; SM00020; tryp_Spc; 1.
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 DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PSS0134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
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 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
 KW signal; Zymogen; EGF-like domain; Repeat; Sulfation; 3D-structure.
 FT SIGNAL 1 23
 FT PROPEP 24 40
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 FT CHAIN 183 492
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 FT CHAIN 234 492
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 FT DOMAIN 86 122
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 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 QY 1 ANGFLXXLRQGSIXRXCXKXIFRXXRTPGFVSY 44
 Db 41 ANSFLXEVKQGNREBLCLEBARVFEADQIDERSWY 84
 RESULT 13
 FAILO RABIT STANDARD; PRT; 490 AA.
 AC 019045;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
 GN F10.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97256311; PubMed=9101642;
 RA Penduth U.R., Anderson K.D., James H.L.,
 RT "Characterization of a full-length cDNA for rabbit factor X.",
 RL Thromb. Res. 85:503-514(1997).
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
 CC converts prothrombin to thrombin in the presence of factor Va,
 CC calcium and phospholipid during blood clotting.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
 CC Arg-|-Ile bonds in prothrombin to form thrombin.
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
 CC MORE DISULFIDE BONDS.
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
 CC CALCIUM (BY SIMILARITY).
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)

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CC (BY SIMILARITY).
CC -1- MISCELLANEOUS; CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
CC EMBL; AF003200; AAB62542.1; -.
CC HSRP; P00742; 1HCG.
CC -----
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR001254; Ser_protease_Try.
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CC SMART; SM00179; EGF_CA; 1.
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CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
CC Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
CC Signal; Zymogen; EGF-like domain; Repeat.
CC SIGNAL; 1 20
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CC MOD_RES 66 66
CC MOD_RES 69 69

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FT MOD_RES 103 103 HYDROXYLATION (BY SIMILARITY).
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FT DISULFID 95 110 BY SIMILARITY.
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FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 244 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
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FT DISULFID 413 441 BY SIMILARITY.
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FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 49.0%; Score 94; DB 1; Length 430;
Best Local Similarity 38.6%; Pred. No. 2,2e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSILRXCRXKLCSEFXAHXIRNXXRTQFVSY 44
Db 41 ANSFLEELKGNLRECEWENCSYEALVEFDEDEKXMEFNKY 84

RESULT 14
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AC 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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GN F9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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RP SEQUENCE FROM N.A.
RX MEDLINE=8600558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antihemophilic
RT factor B).";
RL Biochemistry 24:3736-3750(1985).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham J.B., Stafford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
RT human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236100; PubMed=6329734;
RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
RA Huddleston J.A., Brownlee G.G.;
RT "The gene structure of human anti-haemophilic factor IX.";
RL EMBO J. 3:1053-1060(1984).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=83220788; PubMed=6687940;

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RA Jaye M., de la Salle H., Schamber F., Balland A., Kohli V.,
 RA Finkel A., Tolstoshev P., Lecocq J.P.;
 RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a
 RT unique 5'-base synthetic oligonucleotide probe deduced from the amino
 RT acid sequence of bovine factor IX.";
 RU Nucleic Acids Res. 11:325-235 (1983).
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANTS THR-194 AND PRO-461.
 RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
 RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;
 RU Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 36-326 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=84300526; PubMed=6089357;
 RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;
 RT "Isolation and characterization of human factor IX cDNA:
 RT identification of Tag I polymorphism and regional assignment.";
 RU Somat. Cell Mol. Genet. 10:465-473 (1984).
 RN [7]
 RP SEQUENCE OF 290-359 FROM N.A.
 RX MEDLINE=88127096; PubMed=3340835;
 RA Scofield E.S., Koebler D.D., Sarkar G., Sommer S.S.;
 RT "Genomic amplification with transcript sequencing.";
 RU Science 239:491-494 (1988).
 RN [8]
 RP SEQUENCE OF 444-461 FROM N.A.
 RX MEDLINE=94054330; PubMed=8236150;
 RA de la Salle C., Chantantier J.L., Baas M.J., Schwartz A.,
 RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;
 RT "A deletion located in the 3' non translated part of the factor IX
 RT gene responsible for mild haemophilia B.";
 RU Thromb. Haemost. 70:370-371 (1993).
 RN [9]
 RP SEQUENCE OF 47-461 (VARIANT NAGOYA).
 RX MEDLINE=90078223; PubMed=2592373;
 RA Suehito K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,
 RA Ometa K., Kamiya T., Saito H., Niho Y., Iwanaga S.;
 RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by
 RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell
 RT chymase.";
 RU J. Biol. Chem. 264:21257-21265 (1989).
 RN [10]
 RP HYDROXYLATION OF ASP-110.
 RX MEDLINE=83308813; PubMed=6688526;
 RA McMullen B.A., Fujikawa K., Kissel W.;
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
 RT K-dependent blood coagulation zymogens.";
 RU Biochem. Biophys. Res. Commun. 115:8-14 (1983).
 RN [11]
 RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=78194509; PubMed=659613;
 RA di Sciopio R.G., Kurachi K., Davie E.W.;
 RT "Activation of human factor IX (Christmas factor).";
 RU J. Clin. Invest. 61:1528-1538 (1978).
 RN [12]
 RP CALCULUM-BINDING DATA.
 RX MEDLINE=84185715; PubMed=6425296;
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
 RT "Derivatives of blood coagulation factor IX contain a high affinity
 RT Ca²⁺-binding site that lacks gamma-carboxyglutamic acid.";
 RU J. Biol. Chem. 259:5698-5704 (1984).
 RN [13]
 RP ERRATUM.
 RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;
 RU J. Biol. Chem. 260:2583-2583 (1985).
 RN [14]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=86189947; PubMed=3009023;
 RA Bertley A.K., Rees D.U.G., Rizza C., Brownlee G.G.;
 RT "Defective propeptide processing of blood clotting factor IX caused
 RT by mutation of arginine to glutamine at position -4.";
 RU Cell 45:343-348 (1986).

RN [15]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=90062160; PubMed=2511201;
 RA Nishimura H., Kawabata S., Kissel W., Hase S., Ikenaka T., Takao T.,
 RA Shimonishi Y., Iwanaga S.;
 RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide
 RT (Xyl₂-Glc) O-glycosidically linked to a serine residue in the first
 RT epidermal growth factor-like domain of human factors VII and IX and
 RT protein Z and bovine protein Z.";
 RU J. Biol. Chem. 264:20320-20325 (1989).
 RN [16]
 RP STRUCTURE OF CARBOHYDRATE ON SER-99.
 RX MEDLINE=91344709; PubMed=2129367;
 RA Iwanaga S., Nishimura H., Kawabata S., Kissel W., Hase S., Ikenaka T.,
 RT "A new trisaccharide sugar chain linked to a serine residue in the
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";
 RU Adv. Exp. Med. Biol. 281:121-131 (1990).
 RN [17]
 RP STRUCTURE OF CARBOHYDRATE ON SER-107.
 RX MEDLINE=92388094; PubMed=1517205;
 RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;
 RT "Human factor IX has a tetrasaccharide O-glycosidically linked to
 RT serine 61 through the fucose residue.";
 RU J. Biol. Chem. 267:17520-17525 (1992).
 RN [18]
 RP PHOSPHORYLATION OF SER-114.
 RA Harris R.J., Papac D.I., Truong L., Smith K.J.;
 RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";
 RU (in) Abstracts of 11th International conference on methods in protein
 RN structure analysis, pp.50-50, Annecy (1996).
 RN [19]
 RP POST-TRANSLATIONAL MODIFICATIONS.
 RX MEDLINE=20575397; PubMed=11133752;
 RA Arruda V.R., Hagstrom J.N., Delch J., Heiman-Patterson T.,
 RA Camile R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,
 RA Larson P.J., High K.A.;
 RT "Posttranslational modifications of recombinant mycobute-synthesized
 RT human factor IX.";
 RU Blood 97:130-138 (2001).
 RN [20]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=95229607; PubMed=7718897;
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
 RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane
 RT binding region of factor IX by two-dimensional NMR spectroscopy.";
 RU J. Biol. Chem. 270:7980-7987 (1995).
 RN [21]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=96032604; PubMed=7547952;
 RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;
 RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich
 RT domain of factor IX.";
 RU Biochemistry 34:12126-12137 (1995).
 RN [22]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=96279169; PubMed=8663165;
 RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,
 RA Furie B.;
 RT "Identification of the phospholipid binding site in the vitamin K-
 RT dependent blood coagulation protein factor IX.";
 RU J. Biol. Chem. 271:16227-16236 (1996).
 RN [23]
 RP STRUCTURE BY NMR OF 47-93.
 RX MEDLINE=97199336; PubMed=9047312;
 RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,
 RA Smith H., Hickey R.G., Pedersen L.G.;
 RT "Refinement of the NMR solution structure of the
 RT gamma-carboxyglutamic acid domain of coagulation factor IX using
 RT molecular dynamics simulation with initial Ca²⁺ positions determined
 RT by a genetic algorithm.";
 RU Biochemistry 36:2132-2138 (1997).
 RN [24]
 RP STRUCTURE BY NMR OF 91-133.

RX MEDLINE=91308127; PubMed=1854745;
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;
 RT "Sequence-specific 1H NMR assignments, secondary structure, and
 RT location of the calcium binding site in the first epidermal growth
 RT factor like domain of blood coagulation factor IX.";
 RL Biochemistry 30:7402-7409(1991).
 RN [25]
 RP STRUCTURE BY NMR OF 92-130.
 RX MEDLINE=93284090; PubMed=1304885;
 RA Baton M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,
 RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;
 RT "The three-dimensional structure of the first EGF-like module of
 RT human factor IX: comparison with EGF and TGF-alpha.";
 RL Protein Sci. 1:81-90(1992).
 RN [26]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.
 RX MEDLINE=95330802; PubMed=7606779;
 RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;
 QY Query Match 48.4%; Score 93; DB 1; Length 461;
 Best Local Similarity 41.9%; Pred. No. 3.2e-09;
 Matches 18; Conservative 4; Mismatches 22; Indels 0; Gaps 0;
 Db 2 NGFLXLRQGSIXRCXRLGSPFXAXHIFRXXTTRQFWYSY 44
 49 SGKLEFVQGNLERCEMEKCSFEERAREVENTERTEFTFWKQY 91
 RESULT 15
 PRTC HUMAN STANDARD; PRT; 461 AA.
 AC P04070; Q15189; Q15190; Q16001;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
 DE (Anticlottrudin IIA) (Anticoagulant protein C) (Blood coagulation
 DE factor XIV).
 GN PROC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RX MEDLINE=85270390; PubMed=2991887;
 RA Foster D.C., Yoshitake S., Davie E.W.;
 RT "The nucleotide sequence of the gene for human protein C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85269639; PubMed=2991859;
 RA Beckmann R.J., Schmidt R.J., Sauter R.F., Plutsky J., Crabtree G.R.,
 RA Long G.L.;
 RT "The structure and evolution of a 461 amino acid human protein C
 RT precursor and its messenger RNA, based upon the DNA sequence of
 RT cloned human liver cDNAs.";
 RL Nucleic Acids Res. 13:5233-5247(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120978; PubMed=351171;
 RA Plutsky J., Hosking J.A., Long G.L., Crabtree G.R.;
 RT "Evolution and organization of the human protein C gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Kieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 106-461 FROM N.A.
 RX MEDLINE=86272714; PubMed=6589623;
 RA Foster D.C., Davie E.W.;

RT "Characterization of a cDNA coding for human protein C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
 RN [6]
 RP CARBOHYDRATE-LINKAGE SITE ASN-371.
 RX MEDLINE=90293094; PubMed=1694179;
 RA Miletich J.P., Broze G.J. Jr.;
 RT "Beta protein C is not glycosylated at asparagine 339. The rate of
 RT translation may influence the frequency of usage at asparagine-X-
 RT cysteine sites.";
 RL J. Biol. Chem. 265:11397-11404(1990).
 RN [7]
 RP HYDROXYLATION.
 RX MEDLINE=92184750; PubMed=1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor
 RT domain of factor XII but not protein C.";
 RL J. Biol. Chem. 267:5102-5107(1992).
 RN [8]
 RP 3D-STRUCTURE MODELING OF 175-450.
 RX MEDLINE=94272342; PubMed=8003977;
 RA Fisher C.L., Greengard J.S., Griffin J.H.;
 RT "Models of the serine protease domain of the human antithrombotic
 RT plasma factor activated protein C and its zymogen.";
 RL Protein Sci. 3:588-599(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
 RX MEDLINE=97157472; PubMed=9003757;
 RA Mather T., Oganesyan V., Hof P., Huber R., Foundling S., Esmen C.,
 RA Bode W.;
 RT "The 2.8 A crystal structure of Glu-domainless activated protein C.";
 RL EMBO J. 15:6822-6831(1996).
 RN [10]
 RP REVIEW ON PROC VARIANTS.
 RX MEDLINE=93190290; PubMed=8446940;
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
 RA Sala N., Cooper D.N.;
 RT "Protein C deficiency: a database of mutations. For the Protein C & S
 RT Subcommittee of the Scientific and Standardization Committee of the
 RT International Society on Thrombosis and Hemostasis.";
 RL Thromb. Haemost. 69:77-84(1993).
 RN [11]
 RP VARIANT CYS-444.
 RX MEDLINE=87204221; PubMed=2437584;
 RA Romeo G., Haasan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
 RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
 RA Cortese R.;
 RT "Hereditary thrombophilia: identification of nonsense and missense
 RT mutations in the protein C gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
 RN [12]
 RP VARIANT TRP-211 (LONDON-1).
 RX MEDLINE=90098906; PubMed=2602169;
 RA Grundy C.B., Chittolile A., Talbot S., Bevan D., Kakkar V.V.,
 RA Cooper D.N.;
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
 RT the protein C gene causing thrombosis.";
 RL Nucleic Acids Res. 17:10513-10513(1989).
 RN [13]
 RP VARIANT CYS-272.
 RX MEDLINE=91329836; PubMed=1868249;
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with
 RT symptomatic protein C deficiency type I: heterogeneity and founder
 RT effects.";
 RL Blood 78:890-894(1991).
 RN [14]
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.
 RX MEDLINE=92190481; PubMed=1347706;
 RA Boviell E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,
 RA Rainville I.R., Long G.L.;
 RT "Protein C Vermont: symptomatic type II protein C deficiency
 RT associated with two Glu domain mutations.";
 RL Blood 79:1456-1465(1992).

RN [15]
 RP VARIANT ASP-418 (HONG KONG-2).
 RX MEDLINE=92305321; PubMed=1611081;
 RA Suwahara Y., Miura O., Yuen P., Aoki N.;
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and
 RT a missense mutation.";
 RL Blood 80:126-133(1992).
 RN [16]
 RP VARIANT LEU-289.
 RX MEDLINE=92380660; PubMed=1511988;
 RA Grundy C.B., Christolm M., Kakkar V.V., Cooper D.N.;
 RT "A novel homozygous missense mutation in the protein C (PROC) gene
 RT causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:683-684(1992).
 RN [17]
 RP VARIANTS GLN-220 AND TRP-220.
 RX MEDLINE=92380661; PubMed=1511989;
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)
 RT gene causing recurrent venous thrombosis.";
 RL Hum. Genet. 89:685-686(1992).
 RN [18]
 RP VARIANT GLN-220.
 RX MEDLINE=93250852; PubMed=1301959;
 RA Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,
 RA Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.;
 RT "Two novel mutations responsible for hereditary type I protein C
 RT deficiency: characterization by denaturing gradient gel
 RT electrophoresis.";
 RL Hum. Mutat. 1:491-500(1992).
 RN [19]
 RP VARIANT SER-334.
 RX MEDLINE=92276939; PubMed=1593215;
 RA Yamamoto K., Matsuenita T., Sugitara I., Takamatsu J., Iwasaki E.,
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;
 RT "Homozygous protein C deficiency: identification of a novel missense
 RT mutation that causes impaired secretion of the mutant protein C.";
 RL J. Lab. Clin. Med. 119:682-689(1992).
 RN [20]
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.
 RX MEDLINE=93313192; PubMed=8324221;
 RA Gandrille S., Alhenc-Gelas M., Gausem P., Aillaud M.-F., Dupuy E.,
 RA Juhan-Vaque I., Alach M.;
 RT "Five novel mutations located in exons III and IX of the protein C
 RT gene in patients presenting with defective protein C anticoagulant
 RT activity.";
 RL Blood 82:159-168(1993).
 RN [21]
 RP VARIANTS GLY-14; GLN-211; TYR-244; GLN-253; LEU-321; CYS-328; ILE-385;
 RP THR-388 AND VAL-388.
 RX MEDLINE=93271391; PubMed=8499565;
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
 RA Bertina R.M.;
 RT "Twelve novel and two recurrent mutations in 14 Austrian families
 RT with hereditary protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).
 RN [22]
 RP VARIANT TRP-57.
 RX MEDLINE=93271396; PubMed=8499568;
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,
 RA Kakkar V.V., Cooper D.N.;
 RT "A Glu domain mutation (Arg 15-->Trp) in the protein C (PROC) gene
 RT causing type 2 protein C deficiency and recurrent venous
 RT thrombosis.";
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).
 RN [23]
 RP VARIANTS ARG-145; LEU-210; TRP-211; THR-243; LEU-321; MET-340 AND
 RP TYR-426.
 RX MEDLINE=94122329; PubMed=8292730;
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,
 RA Koepfer M.A., Coughlin J., Griffin J.H.;
 RT "Genetic mutations in ten unrelated American patients with

RT symptomatic type 1 protein C deficiency.";
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).
 RN [24]
 RP VARIANT SER-423.
 RX MEDLINE=94001606; PubMed=8398832;
 RA Marchetti G., Patrascu P., Gemmati D., Caetaman G., Rodeghiero F.,
 RA Macey A., Cooper D.N., Tuddenham E.G., Bernardi F.;
 RT "Symptomatic type II protein C deficiency caused by a missense
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";
 RL Br. J. Haematol. 84:285-289(1993).
 RN [25]
 Query Match 47.4%; Score 91; DB 1; Length 461;
 Best Local Similarity 46.3%; Pred. No. 7.4e-09;
 Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;
 Oy 1 ANGFLXXLRGSLXRYCRXXLCSPFXAAXIFRNXXXTROFW 41
 Db 43 ANSFLELRHSSLERECIERICDFEAKEIFQWVDTLAFW 83
 Search completed: July 28, 2003, 12:24:28
 Job time : 14.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:25 ; Search time 61 seconds
(without alignments)
186.136 Million cell updates/sec

Title: SEQ4
Perfect score: 192
Sequence: 1 ANGFLXXLRGSLXRCRX.....XXAHXIFRNXXRTQFWVSY 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	64.1	701	Q96P08	Q96p08 homo sapien
2	113	58.9	268	Q8NEK6	Q8neke6 homo sapien
3	107	55.7	460	Q91WN8	Q91wn8 mus musculu
4	106	55.2	229	13 Q8JUD0	Q8j140 xenopus lae
5	106	55.2	446	11 Q61109	Q61109 mus musculu
6	105	54.7	231	4 Q8N2N6	Q8n2n6 mus musculu
7	105	54.7	443	13 Q8JHC9	Q8jhc9 brachydanto
8	101	52.6	446	11 Q99PC6	Q99pc6 mus musculu
9	98	51.0	446	11 Q8K3U6	Q8k3u6 mus musculu
10	98	51.0	456	6 Q9TR0	Q9tr0 canis fami
11	96	50.0	482	4 Q63207	Q63207 rattus norv
12	93	48.4	456	4 Q14316	Q14316 homo sapien
13	93	48.4	461	6 Q95ND7	Q95nd7 pan troglod
14	93	48.4	461	6 Q95ND6	Q95nd6 pan troglod
15	93	48.4	481	11 Q54740	Q54740 mus musculu
16	93	48.4	481	11 Q99L32	Q99l32 mus musculu

17	93	48.4	481	11 Q88947	Q88947 mus musculu
18	89	46.4	49	6 Q95ME8	Q95me8 bos taurus
19	89	46.4	469	6 Q9GMD9	Q9gmd9 ornithoxym
20	82	42.7	138	6 Q28994	Q28994 sus scrofa
21	80	41.7	100	4 Q15253	Q15253 homo sapien
22	80	41.7	433	13 Q8JHD0	Q8jhd0 brachydanto
23	80	41.7	433	13 Q90YK1	Q90yk1 brachydanto
24	80	41.7	608	13 Q9PTW7	Q9ptw7 struthio ca
25	80	41.7	648	6 Q29094	Q29094 sus scrofa
26	79	41.1	241	11 Q8CT01	Q8ct01 mus musculu
27	79	41.1	359	11 Q9CQW3	Q9cqW3 mus musculu
28	77	40.1	55	4 Q8J002	Q8j002 homo sapien
29	77	40.1	55	4 Q8IXB5	Q8ixb5 homo sapien
30	76.5	39.8	542	5 Q8TE13	Q8te13 halocynthia
31	75	39.6	474	13 Q8JHC8	Q8jhc8 brachydanto
32	75	39.1	650	4 Q16519	Q16519 homo sapien
33	75	39.1	650	4 Q9NSD0	Q9nsd0 homo sapien
34	71	37.0	179	4 Q8TAS3	Q8tas3 homo sapien
35	71	37.0	198	11 Q8R182	Q8r182 mus musculu
36	68	35.4	376	13 P83370	P83370 holocephal
37	68	35.4	607	13 Q91001	Q91001 gallus gall
38	66	34.4	503	13 Q8AYE4	Q8aye4 brachydanto
39	65	33.9	52	4 Q8IXD5	Q8ixd5 homo sapien
40	64	33.3	678	4 Q14393	Q14393 homo sapien
41	63	32.8	52	4 Q8IXC5	Q8ixc5 homo sapien
42	63	32.8	673	11 Q61592	Q61592 mus musculu
43	63	32.8	674	11 Q99K57	Q99k57 mus musculu
44	62	32.3	226	11 Q8BX25	Q8bx25 mus musculu
45	62	32.3	226	11 Q8BGN6	Q8bgn6 mus musculu

ALIGNMENTS

RESULT 1

Q96P08 PRELIMINARY; PRT; 701 AA.

Q96P08
ID Q96P08
AC Q96P08
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Factor VII active site mutant immunocjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_taxonomy:9606;
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.,
RT "targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AF272774; AKS8686.1; --
DR HSSP: P00761; 1AN1.
DR InterPro: IPR00152; Asx_hydroxy1.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR001438; EGF_T1.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF 2.
DR Pfam: PF00594; gla/ 1.
DR Pfam: PF00047; ig/ 2.
DR Pfam: PF00089; trypsin/ 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLO0D.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGCL; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42C992F CRC64;

Query Match 64.1%; Score 123; DB 4; Length 701;
Best Local Similarity 52.3%; Pred. No. 5.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSGSLKXCRXXLCSFXXAHXIFRNXXRTQFWVS 44
Db 61 ANAFLEELRPSGLERCKEKECCSFEEAREIFKDAERTKLFWISY 104

RESULT 2

Q8NEK6 PRELIMINARY; PRT; 268 AA.
AC Q8NEK6;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Proline-rich Gla (G-carboxyglutamic acid) polypeptide 1
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC030786; AAH30786.1; -;
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLO0D.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
FT NON_TER
SQ SEQUENCE 268 AA; 30295 MW; C3A47C2D9D0007739 CRC64;

Query Match 58.9%; Score 113; DB 4; Length 268;
Best Local Similarity 40.9%; Pred. No. 1.6e-12;
Matches 18; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSGSLKXCRXXLCSFXXAHXIFRNXXRTQFWVS 44
Db 71 ANGFEELRQGNIEHCKEKECTFEAREAREFENNEKTEFWISY 114

RESULT 3

Q91WN8 PRELIMINARY; PRT; 460 AA.
AC Q91WN8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Similar to protein C.

GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; BC013896; AAH13896.1; -.
DR HSSP; M0761; IAN1.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLO0D.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_2; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 460 AA; 51818 MW; 0117F26E8FCC274 CRC64;

Query Match 55.7%; Score 107; DB 11; Length 460;
Best Local Similarity 45.5%; Pred. No. 3.6e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSGSLKXCRXXLCSFXXAHXIFRNXXRTQFWVS 44
Db 42 ANSFLBEMRPSGLERCKEKEICTPEEAQOEIFQVEDTLFWIKY 85

RESULT 4

Q8UJ40 PRELIMINARY; PRT; 229 AA.
AC Q8UJ40;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Mitotic phosphoprotein 77 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21676254; PubMed=11818060;
RA Georgi A.B., Stukenberg P.T., Kirschner M.W.;
RT "Timing of events in mitosis.";
RL Curr. Biol. 12:105-114(2002).
DR EMBL; AF419154; AAM33249.1; -;
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLO0D.

DR PRINTS; PR00001; GLABLO0D.

DR SMART; 2500069; GLA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR NCN TER 229
 DR SEQUENCE 229 AA; 25543 MW; 42A2856BA8A6A9 CRC64;

Query Match 55.2%; Score 106; DB 13; Length 229;
 Best Local Similarity 38.6%; Pred. No. 2.8e-11;
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLKRXCRXXLCSPXXAHXIFRNXXRTROFWVS 44
 Db 21 ANSFLERIKQGNTERECKEELCTYEAREAFENDEKTEPWKEY 64

RESULT 5

ID 061109 PRELIMINARY; PRT; 446 AA.
 AC 061109;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Coagulation factor VII.
 GN F7 OR FVII.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=96276538; Pubmed=8701412;
 RA Iidusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,
 RA Castellino F.J.;
 RL "Characterization of a cDNA encoding murine coagulation factor VII.",
 CC Thromb. Haemost. 75:481-487(1996).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; U44795; AAC52570.1; -
 DR HSSP; P08709; 1PAK.
 DR MGD; MGI:109325; P7.
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; clypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Src; 1.
 DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00025; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01187; EGF CA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-Like domain; Hydroxylase; Protease; Serine protease.
 KM EGF-Like domain; Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 55.2%; Score 106; DB 11; Length 446;
 Best Local Similarity 47.7%; Pred. No. 5.3e-11;
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLKRXCRXXLCSPXXAHXIFRNXXRTROFWVS 44

Db 42 ANSLBELWPGSLERECNEQCSFEAREIFKSPERTKQFWIY 85

RESULT 6

ID 06N2N6 PRELIMINARY; PRT; 231 AA.
 AC 06N2N6;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein FLJ90093.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Isegai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Makamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK074574; BAC11069.1; -
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00594; gla; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00069; GLA; 1.
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 231 AA; 25844 MW; 8A373BD5C1DD081 CRC64;

Query Match 54.7%; Score 105; DB 4; Length 231;
 Best Local Similarity 40.9%; Pred. No. 4.2e-11;
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLKRXCRXXLCSPXXAHXIFRNXXRTROFWVS 44
 Db 20 ANSFLERIKQGNTERECMERICSEYEVKEFENKERTPEWKQY 63

RESULT 7

ID 08JHC9 PRELIMINARY; PRT; 443 AA.
 AC 08JHC9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Coagulation factor VIII.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hannanathiah R., Day K., Jagadeeswaran P.;
 RT "Comprehensive analysis of blood coagulation pathways in Teleostei:
 RT Evolution of coagulation factor genes and identification of zebrafish
 RT factor VIII.";
 RL Blood Cells Mol. Dis. 0:0-0(2002).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AF519546; AAW88342.1; -
 DR EMBL; AF515269; AAN71000.1; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF_2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW SEQUENCE 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;
 SQ

Query Match 54.7%; Score 105; DB 13; Length 443;
 Best Local Similarity 39.5%; Pred. No. 8e-11;
 Matches 17; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Oy 2 NGFLXLRQSLKRCXKXLCSPXAXHIFRNXXRTROPWVS 44
 Db 40 SGFLEMRPGSLRECHMEICDLEFAQETFGVBDTLAFWIKY 82

RESULT 8

ID 099PC6 PRELIMINARY; PRT; 460 AA.
 AC 099PC6
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Anticoagulant protein C.
 GN PROC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL;
 RA Kofl 1;
 RT "Complete sequence of UC72A01."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AF318182; AAK07918.1; -.
 DR HSSP; P04070; LAUT.
 DR MGD; MGI:97771; Proc.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Ca.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW SEQUENCE 446 AA; 50399 MW; 292985EBF119C0HA CRC64;
 SQ

DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW SEQUENCE 460 AA; 51784 MW; 0293BC25B9D3ED16 CRC64;
 SQ

Query Match 52.6%; Score 101; DB 11; Length 460;
 Best Local Similarity 43.2%; Pred. No. 4.6e-10;
 Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSLKRCXKXLCSPXAXHIFRNXXRTROPWVS 44
 Db 42 ANSFLEMRPGSLRECHMEICDLEFAQETFGVBDTLAFWIKY 85

RESULT 9

ID 08K3U6 PRELIMINARY; PRT; 446 AA.
 AC 08K3U6
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Coagulation factor VII.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Murphy K.; Ramaker M.;
 RT "Nucleotide sequence of the cDNA encoding rat coagulation factor VII."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AF532184; AAM95967.1; -.
 DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR000294; Vltk_dep_GLA.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00594; gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00010; EGFBLLOOD.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF_2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR EGF-like domain; Hydrolase; Protease; Serine protease.
 KW SEQUENCE 446 AA; 50399 MW; 292985EBF119C0HA CRC64;
 SQ

Query Match 51.0%; Score 98; DB 11; Length 446;
 Best Local Similarity 45.5%; Pred. No. 1.6e-09;
 Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSLKRCXKXLCSPXAXHIFRNXXRTROPWVS 44
 Db 42 ANSFLEMRPGSLRECHMEICDLEFAQETFGVBDTLAFWIKY 85

DB 42 ANSLBELMSSSLERECNEERCSFEAREIFKSPERTKQFWIT 85

RESULT 10

Q97TR0 ID 097TR0 PRELIMINARY; PRT; 456 AA.

AC Q97TR0; 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Protein C precursor.

OS PROC.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Leeb T., Kopp T., Deppe A., Breen M., Mattis U., Brunberg L.,

RT "Molecular characterization and chromosomal assignment of the canine

RT protein C gene.";

RL Mamm. Genome 10:135-139(1999).

RN [2]

RX SEQUENCE FROM N.A.

RX MEDLINE=99371952; PubMed=10443005;

RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breenig B.,

RT "Analysis of canine protein C gene polymorphisms.";

RL Anim. Genet. 30:237-238(1999).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL: AJ001979; CA05126.1; -.

DR HSSP: P04070; 1AUT.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR001254; Ser_protease_Try.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam: PF00008; EGF_2.

DR Pfam: PF00594; Gla_1.

DR Pfam: PF00089; trypsin_1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00181; EGF_2.

DR SMART: SM00069; GLA_1.

DR SMART: SM00020; TRYD_SPC; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS00011; GLU CARBOXYLATION; 1.

DR PROSITE: PS50240; TRYPsin DOM; 1.

DR PROSITE: PS00134; TRYPsin_HIS; 1.

DR PROSITE: PS00135; TRYPsin_SER; 1.

KW EGF-like domain; Hydroxylase; Protease; Serine protease; Signal.

FT SIGNAL 1 42

FT CHAIN 1 192

FT CHAIN 193 194

FT CHAIN 195 456

FT CHAIN 195 456

SEQUENCE 456 AA; 50813 MW; 7AD3A6C1C34E59FF CRC64;

Query Match 51.0%; Score 98; DB 6; Length 456;

Best Local Similarity 43.2%; Pred. No. 1.6e-09;

Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXRQSLXRCXKXLCSPXAXHIFRNXXRTQFWVSY 44

DB 43 ANSFLERIRAGSLERECNEERCSFEAREIFKSPERTKQFWIT 86

RESULT 11

063207 ID 063207 PRELIMINARY; PRT; 482 AA.

AC 063207; 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Factor X.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=96083366; PubMed=8578539;

RA Stanton C., Ross R.P., Hutson S., Wallin R.,

RT "Evidence for competition between vitamin K-dependent clotting factors

RT for intracellular processing by the vitamin K-dependent gamma-

RT carboxylase.";

RL Thromb. Res. 80:63-73(1995).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL: X79807; CA56202.1; -.

DR HSSP: P00742; 1XKA.

DR MEROPS: S01.216; -.

DR InterPro: IPR000152; Asx_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000742; EGF_2.

DR InterPro: IPR001881; EGF_Ca.

DR InterPro: IPR001438; EGF_I1.

DR InterPro: IPR006209; EGF_like.

DR InterPro: IPR002383; GLA_blood.

DR InterPro: IPR001254; Ser_protease_Try.

DR InterPro: IPR000294; VitK_dep_GLA.

DR Pfam: PF00008; EGF_2.

DR Pfam: PF00594; Gla_1.

DR Pfam: PF00089; trypsin_1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00010; GLABLOOD.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00179; EGF_CA; 1.

DR SMART: SM00069; GLA_1.

DR SMART: SM00020; TRYD_SPC; 1.

DR PROSITE: PS00010; ASX_HYDROXYL; 1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 2.

DR PROSITE: PS01187; EGF_CA; 1.

DR PROSITE: PS00011; GLU CARBOXYLATION; 1.

DR PROSITE: PS50240; TRYPsin DOM; 1.

DR PROSITE: PS00134; TRYPsin_HIS; 1.

DR PROSITE: PS00135; TRYPsin_SER; 1.

KW EGF-like domain; Hydroxylase; Protease; Serine protease.

SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 50.0%; Score 96; DB 11; Length 482;

Best Local Similarity 36.4%; Pred. No. 4e-09;

Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXRQSLXRCXKXLCSPXAXHIFRNXXRTQFWVSY 44

DB 41 ANSFFELIKGNLERECNEERCSFEAREIFKSPERTKQFWIT 84

RESULT 12

Q14316 ID 014316 PRELIMINARY; PRT; 456 AA.

AC 014316; 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas

DE disease, HAEMOPHILIA B)) (Factor IX).

GN F9 OR FACTOR IX.

OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RN NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Beltman P.A., Beltina R.M., Ploos van Amstel J.K., Riemens A.,
RA Bret E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICHN.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_IT.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00089; trypsin.1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00669; GLA_1.
DR SMART; SM00020; TRY_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 48.4%; Score 93; DB 4; Length 456;
Best Local Similarity 41.9%; Pred. No. 1.4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRQGSILRXCRXXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 44 SGKLEFVQGNLERECMEKCSFEAREVFENTERTEFFWKQY 86

RESULT 13
Q95ND7 PRELIMINARY; PRT; 461 AA.
ID Q95ND7;
AC Q95ND7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;

```

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RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB062470; BAB58885.1; JOINED.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR HSSP; P00761; IAN1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_IT.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00009; VItK_dep_GLA.
DR Pfam; PF00594; GLA_1.
DR Pfam; PF00089; trypsin.1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00669; GLA_1.
DR SMART; SM00020; TRY_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F7F45 CRC64;

Query Match 48.4%; Score 93; DB 6; Length 461;
Best Local Similarity 41.9%; Pred. No. 1.4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 2 NGFLXLRQGSILRXCRXXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 49 SGKLEFVQGNLERECMEKCSFEAREVFENTERTEFFWKQY 91

RESULT 14
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ID Q95ND6;
AC Q95ND6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB062471; BAB58886.1; JOINED.

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DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR HSSP; P00761; IAN1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01187; EGF_2; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF6585 CRC64;
SQ

Query Match 48.4%; Score 93; DB 6; Length 461;
Best Local Similarity 41.9%; Pred. No. 1.4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLKXLRQGS LKRXCRXXLCSFYXAHXIFRNXXRTQFWVS 44
Db 49 SGKLEEFVQGNLRECEMEKCSFEAREVFEFTEFTEFWFOY 91
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RESULT 15
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AC O54740;
DT 01-JUN-1998 (Tremblere1.06, Created)
DT 01-JUN-1998 (Tremblere1.06, Last sequence update)
DT 01-MAR-2003 (Tremblere1.23, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN P10 OR FA10.
OS Mus musculus (Mouse).
OC Plasmid pBluescript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxonomy=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; IKKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW Plasmid.
FT SIGNAL 1 40
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DESEF9D97AE CRC64;

OY 1 ANGFLKXLRQGS LKRXCRXXLCSFYXAHXIFRNXXRTQFWVS 44
Db 41 ANSFFEFKXGNLRECEMEKCSFEAREVFEFTEFTEFWFOY 84
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Query Match 48.4%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

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Job time : 62 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
188.756 Million cell updates/sec

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Perfect score: 192
Sequence: 1 ANGFLXXLRGSLXRCRX.....XXAHXIPRNXXRTQFWVS 44

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	85.4	44	20	AAV18306
2	164	85.4	44	22	AAB36396
3	127	66.1	44	20	AAV18302
4	126	65.6	44	20	AAV18310
5	124	64.6	44	20	AAV18311
6	123	64.1	44	20	AAV18305
7	123	64.1	44	22	AAB36395
8	123	64.1	401	22	AAB84870
9	123	64.1	401	22	AAB84871

10	123	64.1	406	14	AAR35764	Factor VII (VII).
11	123	64.1	406	18	AAW14509	Modified blood coa
12	123	64.1	406	18	AAW14510	Modified blood coa
13	123	64.1	406	22	AAU77745	Human factor VIIa
14	123	64.1	406	22	AAW52171	Human FVII SEQ ID
15	123	64.1	406	22	AAW52172	Mammalian expresse
16	123	64.1	406	22	AAW52181	Human FVII mutant
17	123	64.1	406	22	AAW52182	Human FVII mutant
18	123	64.1	406	22	AAW52183	Human FVII mutant
19	123	64.1	406	22	AAW52184	Human FVII mutant
20	123	64.1	406	22	AAW52185	Human FVII mutant
21	123	64.1	406	22	AAW52186	Human FVII mutant
22	123	64.1	406	22	AAW52187	Human FVII mutant
23	123	64.1	406	22	AAW52188	Wild-type human b1
24	123	64.1	406	22	AAW52189	Mutant blood coagu
25	123	64.1	406	22	AAW52190	Mutant blood coagu
26	123	64.1	406	22	AAW52191	Mutant blood coagu
27	123	64.1	406	22	AAW52192	Mutant blood coagu
28	123	64.1	406	23	ABW80051	Human coagulation
29	123	64.1	406	23	ABW80052	Human coagulation
30	123	64.1	406	23	ABW80053	Human coagulation
31	123	64.1	406	23	ABW80054	Human coagulation
32	123	64.1	406	23	ABW80055	Human coagulation
33	123	64.1	406	23	ABW80056	Human coagulation
34	123	64.1	406	23	ABW80057	Human coagulation
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36	123	64.1	406	23	ABW80059	Human coagulation
37	123	64.1	406	23	ABW80060	Human coagulation
38	123	64.1	406	23	ABW80061	Human coagulation
39	123	64.1	406	23	ABW80062	Human coagulation
40	123	64.1	406	23	ABW80063	Human coagulation
41	123	64.1	406	23	ABW80064	Human coagulation
42	123	64.1	406	23	ABW80065	Human coagulation
43	123	64.1	406	23	ABW80066	Human coagulation
44	123	64.1	406	23	ABW80067	Human coagulation
45	123	64.1	406	23	ABW80068	Human coagulation

ALIGNMENTS

RESULT 1	
AAV18306	
ID	AAV18306 standard; peptide; 44 AA.
XX	
AC	AAV18306;
XX	
DT	17-AUG-1999 (first entry)
XX	
DE	Bovine factor VII GLA domain.
XX	
KW	GLA domain; vitamin K-dependent protein; clotting disorder;
KM	therapy.
XX	
OS	Bos taurus.
XX	
FH	Key
FT	Misc-difference 1..44
FT	Location/Qualifiers
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX	
PN	MO9920767-A1.
XX	
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98MO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
XX	
PA	(MINU) UNIV MINNESOTA.
XX	
PI	Neisectuen GL;
XX	

DR WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
XX
XX Discloure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 85.4%; Score 164; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 4.5e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44
Db 1 ANGFLXXLRPQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44

RESULT 2
AAB36396
ID AAB36396 standard; peptide; 44 AA.
XX
XX AAB36396;
AC
XX
XX 27-FEB-2001 (first entry)
DT
XX
XX Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.
DE
XX
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KM factor X; prothrombin; enhanced membrane binding affinity;
KM clot formation; thrombolytic; haemostatic; bleeding disorder;
KM thrombosis; clotting disorder; haemophilia A; haemophilia B;
KM liver disease.
XX
XX Bos taurus.
OS
XX
XX WO20006753-A2.
FN
XX
XX 09-NOV-2000.
PD
XX
XX 28-APR-2000; 2000WO-US11416.
PF
XX
XX 29-APR-1999; 99US-0302239.
PR
XX
XX (MINU) UNIV MINNESOTA.
PA
XX
XX Neiseetuen GL;
PI
XX
XX WPI; 2001-007226/01.
DR
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
PT disorders such as thrombosis and hemophilia, comprising modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
XX
XX Discloure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used

CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type bovine factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;

Query Match 85.4%; Score 164; DB 22; Length 44;
Best Local Similarity 97.7%; Pred. No. 4.5e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44
Db 1 ANGFLXXLRPQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44

RESULT 3
AAV18302
ID AAV18302 standard; peptide; 44 AA.
XX
XX AAV18302;
AC
XX
XX 17-AUG-1999 (first entry)
DT
XX
XX Modified GLA domain of vitamin K-dependent protein.
DE
XX
XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
KM therapy.
KM
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX
XX
XX Key Location/Qualifiers
FT Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
FT
XX
XX WO9920767-A1.
PN
XX
XX 29-APR-1999.
PD
XX
XX 20-OCT-1998; 98WO-US22152.
PF
XX
XX 23-OCT-1997; 97US-0955636.
PR
XX
XX (MINU) UNIV MINNESOTA.
PA
XX
XX Neiseetuen GL;
PI
XX
XX WPI; 1999-288309/24.
DR
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
PT acid domain, useful for treating clotting disorders
PT
XX
XX Claim 11; Page 81; 86pp; English.
XX
XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;

Query Match 66.1%; Score 127; DB 20; Length 44;
Best Local Similarity 77.3%; Pred. No. 1.3e-14;
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

PM WO9920767-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-US22152.
XX
PR 23-OCT-1997; 97US-0955636.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 1999-288309/24.
XX
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
PS Disclosure; Page 15; 86pp; English.
XX
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
CC domain. The invention relates to a vitamin K-dependent polypeptide
CC comprising a modified GLA domain containing an amino acid substitution
CC which enhances membrane binding of the modified polypeptide as compared
CC to the native polypeptide. The polypeptide is used to treat a clotting
CC disorder by decreasing or increasing clot formation. Modification of the
CC GLA domain results in a protein which has enhanced membrane binding
CC affinity as compared to the native protein.
XX
SQ Sequence 44 AA;
XX
Query Match 64.1%; Score 123; DB 20; Length 44;
Best Local Similarity 75.0%; Pred. No. 6.4e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Oy 1 ANGFLXXLRQGLXRXCRXXLCSFXXAHXIFRNXXRTROFWVSX 44
1 ANAFLLXLRPGSLRXKCKXXCSPXXARXIFKDXARTRTFWISY 44
Db
RESULT 7
AAB36395
ID AAB36395 standard; peptide; 44 AA.
XX
AC AAB36395;
XX
DT 27-FEB-2001 (first entry)
XX
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
XX
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;
KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
OS Homo sapiens.
XX
PN WO20006753-A2.
XX
PD 09-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11416.
XX
PR 29-APR-1999; 99US-0302239.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Nelsestuen GL;
XX
DR WPI; 2001-007226/01.
XX
PT Novel vitamin K-dependent polypeptide useful for treating clotting

PT disorders such as thrombosis and hemophilia, comprises modified
PT gamma-carboxy glutamic acid domain that enhances membrane binding
PT affinity -
XX
PS Disclosure; Page 12; 81pp; English.
XX
CC The present invention describes a vitamin K-dependent polypeptide (I)
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having
CC at least one amino acid substitution, that enhances membrane binding
CC affinity and the activity of the polypeptide relative to a corresponding
CC native vitamin K-dependent polypeptide and inhibits clot formation.
CC (I) can have thrombolytic and haemostatic activities, and can be used
CC as an inhibitor of clot formation. (I) is useful for decreasing clot
CC formation in a mammal, a factor VII or factor IX containing a modified
CC GLA domain is useful for increasing clot formation and for treating a
CC bleeding disorder, including thrombosis and clotting disorders such as
CC haemophilia A, haemophilia B and liver disease. The present sequence
CC represents a wild type human factor VII GLA domain sequence, given in
CC the exemplification of the present invention.
XX
SQ Sequence 44 AA;
XX
Query Match 64.1%; Score 123; DB 22; Length 44;
Best Local Similarity 75.0%; Pred. No. 6.4e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Oy 1 ANGFLXXLRQGLXRXCRXXLCSFXXAHXIFRNXXRTROFWVSX 44
1 ANAFLLXLRPGSLRXKCKXXCSPXXARXIFKDXARTRTFWISY 44
Db
RESULT 8
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
AC AAB84870;
XX
DT 31-JUL-2001 (first entry)
XX
DE Mutant blood coagulant factor VII (FVII-31).
XX
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutcin.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"
XX
XX JP2001061479-A.
PD 13-MAR-2001.
XX
PF 24-AUG-1999; 99JP-0237610.
XX
PR 24-AUG-1999; 99JP-0237610.
XX
PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX
DR WPI; 2001-310677/33.
DR N-PSDB; AAH19463.
XX
PT Mutant of blood coagulant factor VII, used for substitution therapy in
PT the treatment of hemophilia -
XX
PS Claim 14; Page 20-21; 29pp; Japanese.
XX
CC The present invention relates to mutants of blood coagulant factor VII
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an

CC agent for the substitution therapy of haemophilia inhibitor patients.
 XX Sequence 401 AA;

Query Match 64.1%; Score 123; DB 22; Length 401;
 Best Local Similarity 52.3%; Pred. No. 5.9e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXCRXXLCSFXAXHIFRNXXRTQFWVSY 44
 1 ANAFLEELRPGSLRECKEBCGCFEAREIRKDMERTGLFWISY 44

RESULT 9
 AAB84871
 ID AAB84871 standard; Protein; 401 AA.

AC AAB84871;

DT 31-JUL-2001 (first entry)

DE Mutant blood coagulant factor VII (FVII-39).

DE Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
 mutant; mutant.

OS Homo sapiens.
 OS Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 235..239
 /note= "Wild-type Val-Pro-Gly-Thr-Thr substituted by
 Asp-Arg-Lys-Thr-Leu"

FT Misc-difference 311..317
 /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
 -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"

PN JP2001061479-A.

PD 13-MAR-2001.

PF 24-AUG-1999; 99JP-0237610.

PR 24-AUG-1999; 99JP-0237610.

PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.

DR WPI; 2001-310677/33.

DR N-PSDB; AAH19464.

PT Mutant of blood coagulant factor VII, used for substitution therapy in
 the treatment of hemophilia -

PS Claim 16; Page 23-24; 29pp; Japanese.

CC The present invention relates to mutants of blood coagulant factor VII
 (FVII) or activated blood coagulant factor VII (FVIIa). The present
 CC sequence is one such mutant FVII: VII-39. The mutants can be used as an
 agent for the substitution therapy of haemophilia inhibitor patients.

XX Sequence 401 AA;

Query Match 64.1%; Score 123; DB 22; Length 401;
 Best Local Similarity 52.3%; Pred. No. 5.9e-13;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRGSLRXCRXXLCSFXAXHIFRNXXRTQFWVSY 44
 1 ANAFLEELRPGSLRECKEBCGCFEAREIRKDMERTGLFWISY 44

RESULT 10
 AAR35764

ID AAR35764 standard; protein; 406 AA.

XX AAR35764;

DT 25-MAR-2003 (updated)
 DT 24-SEP-1993 (first entry)

DE Factor VII (VII).

XX PC, protein C; IX, Factor IX; X, Factor X; PT, prothrombin; VII;
 KW Factor VII; CT, chymotrypsinogen; SP, serine protease; binding;
 XX exosite; catalytic activity.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..152
 /note= "Factor VII light chain"

FT Region 153..406
 /note= "Factor VII heavy chain"

FT Peptide 374..388
 /note= "exosite 1"

FT Peptide 290..310
 /note= "exosite 2"

FT Peptide 374..388
 /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 289..304
 /note= "pref. PC polypeptide; claim 2, page 136"

FT Peptide 290..304
 /note= "pref. PC polypeptide; claim 4, page 137"

FT Peptide 245..266
 /note= "claim 9, page 138-139 describes an antibody
 that reacts with Factor VII; fragments
 289-304, 290-310, 374-388 and
 400-414 but not with fragment 245-266"

PN WO9309804-A1.

PD 27-MAY-1993.

PF 18-NOV-1992; 92WO-US10242.

PR 18-NOV-1991; 91US-0793989.

PA (SCRI) SCRIPPS RES INST.

PI Griffin JH, Meesters RM;

DR WPI; 1993-182244/22.

XX Serine protease derived polypeptide(s) and anti-peptide
 PT antibodies - for inhibiting coagulation and assaying for the
 PT presence of serine protease in fluid samples

PS Disclosure; Page 133-135; 149pp; English.

CC The PC polypeptides indicated in the features table inhibit
 CC coagulation (they prevent binding of serine protease to natural
 CC substrates), esp. when admin. to give an intravascular blood
 CC concn. of 0.1-100 (pref. 0.5-10) microm.

CC NB: Sequences corresp. to SEQ ID NO 6, 7, 8 and 9 are described
 CC in the specification but have not yet been added to the SEQUENCE
 CC LISTING.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 406 AA;

Query Match 64.1%; Score 123; DB 14; Length 406;
 Best Local Similarity 52.3%; Pred. No. 6e-13;
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY	1	ANGFLXXLRQSGIXLRXCRRXXLCSFXXAHXIFRXHXTROWWXY	44
DB	1	ANAFLEELRPGSLIERCKEEOCSFEEDAREIFKDAERTKJFWISY	44
RESULT 11			
ID	AAW14509	standard; protein; 406 AA.	
XX	AAW14509;		
AC	25-MAR-2003	(updated)	
DT	14-MAY-1997	(first entry)	
XX	Modified blood coagulation Factor VII (R290S).		
DE	Blood coagulation; factor 7; mutant; mutation; modification; thrombocytopenia; von Willebrand's disease; plasma substitute		
KW	Homo sapiens.		
XX	Synthetic.		
OS	Key	location/Qualifiers	
PH	Modified-site	6	
FT		/label= OTHER	
FT	Modified-site	/note= "gamma-carboxylutamic acid"	
FT		7	
FT	Modified-site	/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	14	
FT		/label= OTHER	
FT	Modified-site	/note= "gamma-carboxylutamic acid"	
FT		16	
FT	Modified-site	/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	19	
FT		/label= OTHER	
FT	Modified-site	/note= "gamma-carboxylutamic acid"	
FT		20	
FT	Modified-site	/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	17..22	
FT		25	
FT	Modified-site	/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	26	
FT		/label= OTHER	
FT	Modified-site	/note= "gamma-carboxylutamic acid"	
FT		29	
FT	Modified-site	/label= OTHER	
FT		/note= "gamma-carboxylutamic acid"	
FT	Modified-site	32..33	
FT		/note= "proteolytic site"	
FT	Modified-site	35	
FT		/label= OTHER	
FT	Modified-site	/note= "gamma-carboxylutamic acid"	
FT		38..39	
FT	Cleavage-site	/note= "proteolytic site"	
FT		42..43	
FT	Cleavage-site	/note= "proteolytic site"	
FT		44..45	
FT	Cleavage-site	/note= "proteolytic site"	
FT		50..61	
FT	Modified-site	55..70	
FT		63	
FT	Modified-site	/label= OTHER	
FT		/note= "beta-hydroxy-aspartic acid"	
FT	Modified-site	72..81	
FT		91..102	
FT	Modified-site	98..112	
FT		114..127	
FT	Modified-site	135..162	
FT		143..164	
FT	Cleavage-site	143..144	

FT			/note= "proteolytic site"
FT	Modified-site	145	
FT		/note= "glycosylation site"	
FT	Dissulfide-bond	159..164	
FT	Dissulfide-bond	178..194	
FT	Active-site	193	
FT	Active-site	242	
FT	Active-site	344	
FT	Cleavage-site	290..291	
FT	Misc-difference	290	
FT		/note= "proteolytic site in unmodified factor VII"	
FT	.	/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"	
FT	Dissulfide-bond	310..329	
FT	Cleavage-site	315..316	
FT		/note= "proteolytic site"	
FT	Modified-site	322	
FT		/note= "glycosylation site"	
FT	Dissulfide-bond	340..368	
FT	Cleavage-site	341..342	
FT		/note= "proteolytic site"	
FT	Cleavage-site	392..393	
FT		/note= "proteolytic site"	
FT	Cleavage-site	396..397	
FT		/note= "proteolytic site"	
FT	Cleavage-site	402..403	
FT		/note= "proteolytic site"	
PX			
PN	US5580560-A.		
XX			
PD	03-DEC-1996.		
XX			
PF	22-AUG-1994;	94US-0293778.	
XX			
PR	09-AUG-1993;	93US-0104509.	
PR	13-NOV-1989;	89US-0434149.	
PR	12-JUN-1992;	92US-0898248.	
PR	22-AUG-1994;	94US-0293778.	
XX	(NOVO) NOVO-NORDISK AS.		
PA			
XX	Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
PI			
XX			
DR	WPI; 1997-033523/03.		
XX			
PT	Mutated human factor VII or VIIA proteins - with amino acid substitutions to improve proteolytic stability		
XX			
PS	Example 3; Page -: 28pp; English.		
XX			
CC	Modified human factor VII or VIIA proteins are stabilised against proteolytic cleavage by substitution of one of the residues Lys32,		
CC	Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and		
CC	Lys431 by an amino acid that provides a proteolytically more stable		
CC	peptide bond, provided that Lys32 is replaced by Gln, Glu, His,		
CC	Gly, Thr, Ala or Ser. The modified proteins are useful for treating		
CC	bleeding disorders such as thrombocytopenia and von Willebrand's		
CC	diseases. They are also suitable for addition to plasma substitutes.		
CC	The present sequence is a specific example of a modified factor VII protein.		
CC	(Updated on 25-MAR-2003 to correct PF field.)		
CC			
SQ	Sequence 406 AA;		
	Query Match 64.1%; Score 123; DB 18; Length 406;		
	Best Local Similarity 52.3%; Pred.No. 6e-13;		
	Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;		
OY	1 ANGFLXLRLQGSLKRCRXHLCISFXXAHKIFRNXXTRGFWMVS Y 44 :: : DB 1 ANAFLEELRPGSLERECCKEQQCFEEAREIFPKDAERTKLFWIS Y 44		

XX	AAU77745;
AC	
XX	05-JUN-2002 (first entry)
DT	
XX	
DE	Human factor VIIa active site mutant.
XX	
KW	Factor VIIa; human; shock heat treatment; protein stability;
KW	protein manufacture; protein conformation; mutant; muteln.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key
FT	Active-site
FT	Location/Qualifiers
FT	193
FT	/note= "Member of the factor VIIa catalytic triad"
FT	Active-site
FT	242
FT	/note= "Member of the factor VIIa catalytic triad"
FT	Active-site
FT	344
FT	/note= "Member of the factor VIIa catalytic triad"
FT	Misc-difference
FT	344
FT	/label= Gly, Met, Thr
FT	/note= "Preferably Ala. Wild type Ser"
XX	
XX	WO200177141-A1.
PN	
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-DK00234.
XX	
PR	06-APR-2000; 2000DK-0000573.
PR	17-APR-2000; 2000US-197650P.
XX	
PA	(NOVO) NOVO NORDISK AS.
XX	
P1	Mathiesen F;
DR	
XX	WPI; 2001-657162/75.
PT	
PT	Stabilisation of a polypeptide e.g. in a pharmaceutical composition
PT	involves a shock heat treatment
XX	
PS	Disclosure; Page -; 22pp; English.
XX	
XX	The invention describes a method of stabilising a polypeptide involving
CC	shock heat treatment of the polypeptide. The method is useful in a
CC	pharmaceutical composition, in the industrial or large scale method of
CC	manufacturing a polypeptide, also as a unit operation during preparation,
CC	purification, recovery and/or formulation of polypeptides. The shock heat
CC	treatment improves the protein stability without substantial loss of
CC	biological activity. The method can be applied to change polypeptide
CC	conformation in a very fast and non-invasive manner. The polypeptide
CC	formed is stable. The method is also useful for decreasing the
CC	association of the polypeptide. This sequence represents a modified
CC	human factor VIIa protein, mutated at the catalytic site, described
CC	in the invention.
CC	Note: This sequence does not appear in the specification but has
CC	been obtained using information given in the invention.
XX	
XX	Sequence 406 AA;
XX	

```

Query Match 64.1%; Score 123; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 66-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0

OY      1 ANGFLXXLRQGS LKRXRCRXXLCSEFYXAHXIFRNXXRTQFWVS Y 44
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1 ANAFLEELRPGLSLERECEQCSFEAEAEIFXDAERTKLFWIS Y 44

RESULT 14
AAMS2171
ID AAMS2171 standard; Protein; 406 AA.

```

XX	AAM52171;
AC	
DT	07-FEB-2002 (first entry)
DE	Human FVII SEQ ID NO 1.
XX	
KW	Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic; cardiac; hepatocellular; cerebroprotective; haemophilia; liver disease; myocardial infarction; thrombotic stroke; deep-vein thrombosis.
OS	Homo sapiens.
XX	
FH	Key
FT	Misc-difference 6
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 7
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 14
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 16
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 19
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 20
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 25
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 26
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 29
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 35
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference 52
FT	/note= "O-glycosylated"
FT	Modified-site 60
FT	/note= "O-glycosylated"
FT	Modified-site 145
FT	/note= "N-glycosylated"
FT	/note= "N-glycosylated" 152..153
FT	"proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Modified-site 322
FT	/note= "N-glycosylated"
PX	WO200158935-A2.
PN	
PD	16-AUG-2001.
XX	
PP	12-FEB-2001, 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218. 18-OCT-2000; 2000DK-0001558.
PA	(MAXY-) MAXYGEN APS.
PI	Andersen KV, Pedersen AH, Bornaes C;
PR	WPI, 2001-581807/65.
PS	N-PSDB; AA19982.

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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:25:31 ; Search time 32.5 Seconds

(without alignments)
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Listing first 45 summaries

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	85.4	44	US-10-298-330-4	Sequence 4, Appl1
2	123	64.1	44	US-10-298-330-3	Sequence 3, Appl1
3	123	64.1	406	US-09-782-5878-1	Sequence 1, Appl1
4	123	64.1	406	US-09-782-5878-3	Sequence 3, Appl1
5	123	64.1	406	US-10-109-498-1	Sequence 1, Appl1
6	123	64.1	406	US-10-255-032-1	Sequence 1, Appl1
7	123	64.1	406	US-10-281-122-1	Sequence 1, Appl1
8	123	64.1	466	US-10-017-122-2	Sequence 2, Appl1
9	104	54.2	40	US-10-298-330-23	Sequence 2, Appl1
10	102	53.1	40	US-10-298-330-26	Sequence 26, Appl1
11	101	52.6	40	US-10-298-330-25	Sequence 25, Appl1
12	98	51.0	40	US-10-298-330-22	Sequence 22, Appl1
13	97	50.5	44	US-10-298-330-2	Sequence 2, Appl1
14	96	50.0	419	US-10-182-263-6	Sequence 6, Appl1
15	95	49.5	40	US-10-298-330-24	Sequence 24, Appl1

16	93	48.4	415	9	US-09-118-748-2	Sequence 2, Appl1
17	93	48.4	461	9	US-09-884-901-3	Sequence 3, Appl1
18	93	48.4	461	15	US-10-132-829-5	Sequence 5, Appl1
19	93	48.4	461	15	US-10-234-406-6	Sequence 6, Appl1
20	93	48.4	461	15	US-10-234-406-8	Sequence 8, Appl1
21	91	47.4	44	15	US-10-298-330-18	Sequence 18, Appl1
22	91	47.4	419	15	US-09-978-917A-4	Sequence 4, Appl1
23	91	47.4	419	15	US-10-182-263-3	Sequence 1, Appl1
24	91	47.4	419	15	US-10-182-263-3	Sequence 3, Appl1
25	91	47.4	419	15	US-10-182-263-3	Sequence 3, Appl1
26	91	47.4	419	15	US-10-182-263-3	Sequence 3, Appl1
27	91	47.4	419	15	US-10-182-263-3	Sequence 3, Appl1
28	91	47.4	461	11	US-09-978-917A-2	Sequence 2, Appl1
29	91	47.4	461	15	US-10-182-263-2	Sequence 2, Appl1
30	89	46.4	45	15	US-10-298-330-5	Sequence 5, Appl1
31	86	44.8	41	15	US-10-298-330-27	Sequence 27, Appl1
32	80	41.7	622	15	US-10-020-141-8	Sequence 8, Appl1
33	80	41.7	622	15	US-10-017-631-2	Sequence 2, Appl1
34	80	41.7	622	15	US-10-214-932-116	Sequence 116, Appl1
35	80	41.7	622	15	US-10-172-712-29	Sequence 29, Appl1
36	78.5	40.9	46	15	US-10-298-330-6	Sequence 6, Appl1
37	73	38.0	44	15	US-10-298-330-19	Sequence 19, Appl1
38	70	36.5	45	15	US-10-298-330-17	Sequence 17, Appl1
39	70	36.5	96	11	US-09-759-130B-313	Sequence 13, Appl1
40	70	36.5	96	15	US-10-189-123-43	Sequence 43, Appl1
41	70	36.5	209	11	US-09-759-130B-312	Sequence 12, Appl1
42	70	36.5	209	15	US-10-189-123-42	Sequence 42, Appl1
43	70	36.5	226	11	US-09-759-130B-310	Sequence 310, Appl1
44	70	36.5	226	15	US-10-189-123-40	Sequence 40, Appl1
45	63	32.8	673	15	US-10-223-085-48	Sequence 48, Appl1

ALIGNMENTS

RESULT 1
US-10-298-330-4
Sequence 4, Application US/10298330
Publication No. US20030100506A1
GENERAL INFORMATION:
APPLICANT: Neleestuen, Gary L.
TITLE OF INVENTION: Modified Vitamin K-Dependent
FILE REFERENCE: 09531-127001
CURRENT APPLICATION NUMBER: US/10/298,330
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/497,591
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/302,239
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 44
TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: VARIANT
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-4

Query Match 85.4%; Score 164; DB 15; Length 44;
Best Local Similarity 97.7%; Pred. No. 4.2e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLXRCXRXLCSPFXAHXIFRNXXRTQFWVSY 44
DB 1 ANGFLXXLRQSLXRCXRXLCSPFXAHXIFRNXXRTQFWVSY 44


```

; SEQ ID NO: 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1
```

```

Query Match          64.1%; Score 123; DB 15; Length 406;
Best Local Similarity 75.0%; Pred. No. 4e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```

Qy      1 ANGFLLXLRQGLRXCRLXKCFXXAHXIFRNXXRTQFWVSY 44
Db      1 ANAFLLXLRPGSLRXCRLXKCFXXAHXIFRDXARTLFWISY 44
```

```

RESULT 6
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A10 No. US20030100075A1disk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255.032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-255-032-1
```

```

Query Match          64.1%; Score 123; DB 15; Length 406;
Best Local Similarity 75.0%; Pred. No. 4e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```

Qy      1 ANGFLLXLRQGLRXCRLXKCFXXAHXIFRNXXRTQFWVSY 44
Db      1 ANAFLLXLRPGSLRXCRLXKCFXXAHXIFRDXARTLFWISY 44
```

```

RESULT 7
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Pelsion, Egon
; APPLICANT: Olsen, Ole Hvalsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; FILE REFERENCE: 6410.200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
```

```

; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1
```

```

Query Match          64.1%; Score 123; DB 16; Length 406;
Best Local Similarity 75.0%; Pred. No. 4e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```

Qy      1 ANGFLLXLRQGLRXCRLXKCFXXAHXIFRNXXRTQFWVSY 44
Db      1 ANAFLLXLRPGSLRXCRLXKCFXXAHXIFRDXARTLFWISY 44
```

```

RESULT 8
US-10-017-122-2
; Sequence 2, Application US/10017122
; Publication No. US20030087244A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MM1-007
; CURRENT APPLICATION NUMBER: US/10/017,122
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/327,487
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-122-2
```

```

Query Match          64.1%; Score 123; DB 15; Length 466;
Best Local Similarity 52.3%; Pred. No. 4.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
```

```

Qy      1 ANGFLLXLRQGLRXCRLXKCFXXAHXIFRNXXRTQFWVSY 44
Db      61 ANAFLEELRPGSLRXCRLXKCFXXAHXIFRDXARTLFWISY 104
```

```

RESULT 9
US-10-298-330-23
; Sequence 23, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelissen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-23
```

Query Match 54.2%; Score 104; DB 15; Length 40;
Best Local Similarity 77.5%; Pred. No. 8.6e-11;
Matches 31; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40
Db 1 ANAFLLXLRQGSILRXCRXXQCSFXXARXIFDXAXRTKLF 40

RESULT 10
US-10-298-330-26
; Sequence 26, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Neleestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 33, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-26

Query Match 53.1%; Score 102; DB 15; Length 40;
Best Local Similarity 77.5%; Pred. No. 1.9e-10;
Matches 31; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40
Db 1 ANAFLLXLRQGSILRXCRXXQCSFXXARXIFDXAXRTKLF 40

RESULT 11
US-10-298-330-25
; Sequence 25, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Neleestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35

; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-25

Query Match 52.6%; Score 101; DB 15; Length 40;
Best Local Similarity 77.5%; Pred. No. 2.8e-10;
Matches 31; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40
Db 1 ANAFLLXLRQGSILRXCRXXQCSFXXARXIFDXAXRTKLF 40

RESULT 12
US-10-298-330-22
; Sequence 22, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Neleestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-22

Query Match 51.0%; Score 98; DB 15; Length 40;
Best Local Similarity 75.0%; Pred. No. 9.3e-10;
Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40
Db 1 ANAFLLXLRQGSILRXCRXXQCSFXXARXIFDXAXRTKLF 40

RESULT 13
US-10-298-330-2
; Sequence 2, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Neleestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus

FEATURE: 1
NAME/KEY: VARIANT
LOCATION: 6, 7, 14, 16, 19, 20, 23, 25, 26, 29, 35
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-2

Query Match 50.5%; Score 97; DB 15; Length 44;
Best Local Similarity 65.9%; Pred. No. 1.5e-09;
Matches 29; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCRXXCSPXXAHXIFRNXXRTROFV 44
DB 1 ANSFLLXXLRPGNVXRCXSVXCXFXAXRIFONTXDTWAFWSFY 44

RESULT 14

US-10-182-263-6
Sequence 6, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Jones, Bruce E
APPLICANT: Gerlitz, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-182-263-6

Query Match 50.0%; Score 96; DB 15; Length 419;
Best Local Similarity 48.8%; Pred. No. 1.9e-08;
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCRXXCSPXXAHXIFRNXXRTROFV 41
DB 1 ANSFLEIRQGSLEKRECIERICDPEBAKEIFEDVDITLAFW 41

RESULT 15

US-10-298-330-24
Sequence 24, Application US/10298330
Publication No. US20030100506A1
GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary L.
TITLE OF INVENTION: Modified Vitamin K-Dependent
Peptides
FILE REFERENCE: 09531-127001
CURRENT APPLICATION NUMBER: US/10/298,330
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/497,591
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/302,239
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 08/955,636
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-24

Query Match 49.5%; Score 95; DB 15; Length 40;
Best Local Similarity 75.0%; Pred. No. 3e-09;
Matches 30; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSIXRCRXXCSPXXAHXIFRNXXRTROF 40
DB 1 ANAFLLXXLRPGSLRXKCKXQCSFXAXRIFDAXRTKLF 40

Search completed: July 28, 2003, 12:38:59
Job time: 32.5 secs

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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:22:40 ; Search time 20 Seconds
(without alignments)
93.084 Million cell updates/sec

Title: SEQ4
Perfect score: 192
Sequence: 1 ANGFLXXLRGSLXRCRX...XXAHXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	85.4	44	3	US-08-955-636-4
2	127	66.1	44	3	US-08-955-636-30
3	126	65.6	44	3	US-08-955-636-26
4	124	64.6	44	3	US-08-955-636-27
5	123	64.1	44	3	US-08-955-636-3
6	123	64.1	406	1	US-08-293-778-24
7	123	64.1	406	1	US-08-295-411-5
8	123	64.1	406	2	US-08-955-471-5
9	123	64.1	406	5	PCT-US92-10242-5
10	123	64.1	444	1	US-08-475-845-2
11	123	64.1	444	2	US-08-327-680-2
12	123	64.1	444	2	US-08-660-289-2
13	123	64.1	444	2	US-08-537-807-2
14	123	64.1	444	2	US-08-871-003-2
15	123	64.1	444	2	US-08-464-233-2
16	123	64.1	444	3	US-09-189-607-2
17	123	64.1	444	3	US-09-378-907-2
18	123	64.1	444	5	PCT-US94-05779-2
19	123	64.1	466	1	US-07-882-202A-4
20	123	64.1	466	1	US-08-021-615A-4
21	123	64.1	466	3	US-08-321-777-4
22	123	64.1	466	3	US-09-009-217-14
23	123	64.1	466	3	US-09-009-656-14
24	123	64.1	466	3	PCT-US93-04493-4
25	122	63.5	44	3	US-08-955-636-28
26	119	62.0	44	3	US-08-955-636-29
27	109	56.8	41	1	US-08-229-280-4

28	101	52.6	139	1	US-08-310-978-2	Sequence 2, Appli
29	101	52.6	139	1	US-08-474-042-2	Sequence 2, Appli
30	101	52.6	139	1	US-08-484-558-2	Sequence 2, Appli
31	101	52.6	139	1	US-08-774-592-2	Sequence 2, Appli
32	101	52.6	437	1	US-08-487-037-2	Sequence 2, Appli
33	101	52.6	437	1	US-08-487-037-3	Sequence 3, Appli
34	101	52.6	488	1	US-08-487-037-1	Sequence 1, Appli
35	98	51.0	44	3	US-08-955-636-23	Sequence 23, Appli
36	97	50.5	44	3	US-08-955-636-2	Sequence 2, Appli
37	96	50.0	44	3	US-08-955-636-24	Sequence 24, Appli
38	96	50.0	448	1	US-08-295-411-3	Sequence 3, Appli
39	96	50.0	448	2	US-08-955-471-3	Sequence 3, Appli
40	96	50.0	448	5	PCT-US92-10068-1	Sequence 1, Appli
41	96	50.0	448	5	PCT-US92-10242-3	Sequence 3, Appli
42	96	50.0	488	4	US-09-367-777-44	Sequence 44, Appli
43	96	50.0	488	4	US-09-367-791A-27	Sequence 27, Appli
44	95	49.5	487	1	US-08-469-486-53	Sequence 53, Appli
45	95	49.5	487	2	US-08-469-658-53	Sequence 53, Appli

ALIGNMENTS

```
RESULT 1
US-08-955-636-4
; Sequence 4, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsaestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      85.4%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3e-22; 1; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 1;

Cy      1 ANGFLXXLRGSLXRCRXLCFFXXAHXIFRNXXRTQFWVSY 44
Db      1 ANGFLXXLRGSLXRCRXLCFFXXAHXIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsaestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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```
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```
Query Match 66.1%; Score 127; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 1.2e-15;
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy 1 ANGFLLXLRQGLXKRCXKXCSFXXAHXIFRNXXRTQFWVS 44
Db 1 ANAFLLXLRQGLXKRCXKXCSFXXAHXIFRDAXRTKLFWISY 44
```

RESULT 3

```
US-08-955-636-26
/ Sequence 26, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelsestuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26
```

```
Query Match 65.6%; Score 126; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.8e-15;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 ANGFLLXLRQGLXKRCXKXCSFXXAHXIFRNXXRTQFWVS 44
Db 1 ANAFLLXLRQGLXKRCXKXCSFXXAHXIFRDAXRTKLFWISY 44
```

RESULT 4

```
US-08-955-636-27
/ Sequence 27, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelsestuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 27
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```
Query Match 64.6%; Score 124; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 4.1e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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```
Qy 1 ANGFLLXLRQGLXKRCXKXCSFXXAHXIFRNXXRTQFWVS 44
Db 1 ANAFLLXLRQGLXKRCXKXCSFXXAHXIFRDAXRTKLFWISY 44
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```
RESULT 5
US-08-955-636-3
/ Sequence 3, Application US/08955636A
/ Patent No. 6017882
/ GENERAL INFORMATION:
/ APPLICANT: Nelsestuen, Gary
/ TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
/ FILE REFERENCE: 09531/002001
/ CURRENT APPLICATION NUMBER: US/08/955,636A
/ CURRENT FILING DATE: 1997-10-23
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 3
/ LENGTH: 44
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
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Query Match 64.1%; Score 123; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 6.1e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 ANGFLLXLRQGLXKRCXKXCSFXXAHXIFRNXXRTQFWVS 44
Db 1 ANAFLLXLRQGLXKRCXKXCSFXXAHXIFRDAXRTKLFWISY 44
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RESULT 6

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US-08-293-778-24
/ Sequence 24, Application US/08293778
/ Patent No. 5580560
/ GENERAL INFORMATION:
/ APPLICANT: Nicolaisen, Else M.
/ APPLICANT: Bjorn, Soren E.
/ APPLICANT: Woberg, Finn C.
/ APPLICANT: Woodbury, Richard
/ TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: No. 5580560o No. 5580560disk of No. 5580560th America, Inc.
/ STREET: 405 Lexington Avenue, 62nd floor
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10174-6201
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/293,778
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/104,509
/ FILING DATE:
/ APPLICATION NUMBER: DK 3235/87
/ FILING DATE: 25-JUN-1987
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/434,149
/ FILING DATE: 13-NOV-1989
/ PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: PCT/DK88/00103
FILING DATE: 24-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,248
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Agis, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3129,224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-293-778-24

Query Match 64.1%; Score 123; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQSLRXCRXXLCSPFXAXHIFRNXXRTROPVSY 44
Db 1 ANAFLEYLRPGSLRYCKYQCSPFYATYITFKDARTLFWISY 44

RESULT 7
US-08-295-411-5
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Office of Patent Counsel, The Scripps
ADDRESSER: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263,0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match 64.1%; Score 123; DB 1; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQSLRXCRXXLCSPFXAXHIFRNXXRTROPVSY 44
Db 1 ANAFLEBLRPGSLERBECKEBCSPFEAREIFKDAERTLFWISY 44

RESULT 8
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Office of Patent Counsel, The Scripps
ADDRESSER: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSR1263,0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 64.1%; Score 123; DB 2; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSIXRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44
1 ANAFLELRPGSLERCKEBCQSPFEAREIFKDAERTKLFWISY 44
Db

RESULT 9
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242

GENERAL INFORMATION:
APPLICANT: Giffin, John H.
APPLICANT: Meesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: For Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pitting, Thomas

REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRO472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:

NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5

Query Match 64.1%; Score 123; DB 5; Length 406;
Best Local Similarity 52.3%; Pred. No. 6.3e-14;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
QY 1 ANGFLXLRQGSIXRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44
1 ANAFLELRPGSLERCKEBCQSPFEAREIFKDAERTKLFWISY 44
Db

RESULT 10
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5786955

GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475, 845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-843-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-475-845-2

Query Match 64.1%; Score 123; DB 1; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSIXRCXKXLCSPFXAXHIFRNXXRTQFWVSY 44
1 ANAFLELRPGSLERCKEBCQSPFEAREIFKDAERTKLFWISY 82
Db

RESULT 11
US-08-327-690-2

```
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match      64.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      1 ANGFLXXLRQSLXKCRXXLCSPFXAHXIFRNXXRTQFWVSY 44
Db      39 ANAFLELRPGSLERBECKEQCFEAREIFKDAERTKLFWISY 82

RESULT 12
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
```

```
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match      64.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      1 ANGFLXXLRQSLXKCRXXLCSPFXAHXIFRNXXRTQFWVSY 44
Db      39 ANAFLELRPGSLERBECKEQCFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 07/662,920
FILING DATE: 28-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-1DC
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-537-807-2

Query Match 64.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLRXCRXXLCSFXXAHXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14
US-08-871-003-2
Sequence 2, Application US/08871003
Patent No. 5937864
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match 64.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLRXCRXXLCSFXXAHXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match 64.1%; Score 123; DB 3; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLRXCRXXLCSFXXAHXIFRNXXRTROFWVS 44
DB 39 ANAFLELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: July 28, 2003, 12:28:21
Job time : 20 secs